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(54) Title: ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES

(57) Abstract: An algorithm has been developed to identify four DNA sequences of 20 bases or more that form a structure called a connectron. Two sequences C1 and C2 are adjacent to each other. These sequences are expressed as RNA in the 3'UTR of some genes in many prokaryotic, archea and eukaryotic genomes. The other half of a connectron is two DNA sequences T1 and T2 that are on the same chromosome and range in distance from each other by about 1kb to 105kb. The C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. C1/C2 and T1-T2 can be on different chromosomes. The C1/C2 RNA sequence of the gene transcript finds the two double-stranded DNA sequences T1 and T2. The single-stranded RNA and double-stranded DNA then form a triple-stranded Hoogsteen helix of the RNA/DNA/DNA variety. Because the C1 sequence is adjacent to the C2 sequence, the T1 sequence is made spatially adjacent to the T2 sequence in a compact X-shaped structure. Chromatin particles form as compact 30nm assemblies in the DNA between T1 and T2 thus eliminating the intervening genes from promotion and expression. Connectrons remove sets of genes from expression and thus modulate the behavior of many types of cells.

ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES

Reference to Related Application

The present application is the subject of Provisional Application Serial No. 60/208,650 filed June 2, 2000 entitled ALGORITHMIC DETERMINATION OF CONNECTRONS FOR THE HIGH LEVEL REGULATION OF GENE EXPRESSION.

Introduction

RNA introduced into a cell by a virus is now known to trigger a cellular defense mechanism known as post-transcriptional gene silencing (PTGS). If the viral RNA sequence matches a sequence within the cell's genome the associated genes are turned off or silenced. This phenomenon is also called 'RNA interference' or RNAi. A single-stranded RNA can interact with another single-stranded RNA (known as antisense RNA). The single-stranded RNA can also form a triple-stranded complex with double-stranded DNA. This triple-stranded complex is known as a Hoogsteen helix. This patent application shows how two specific adjacent RNA single-stranded sequences (called C1 and C2 – for Control Sequence 1 and Control Sequence 2) interact with two distant double-stranded DNA sequences (called T1 and T2 – for Target Sequence 1 and Target Sequence 2) to form a tetradic relationship which is called a "connectron". The two distant DNA double-stranded sequences (T1 and T2) must be on the same chromosome in a genome and they must be between about 1kb and 105kb of each other. The adjacent single-stranded RNA sequences (C1/C2) can be on the same or different chromosome as the T1 and T2 sequences. The C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2

sequence. The connectron acts to stabilize the double-stranded DNA by allowing 30nm chromatin particles to form. Genes that lie between the T1 and T2 sequences when wrapped up in 30nm chromatin particles are not open to promotion and expression. The connectron (i.e. the tetradic relationship between the T1-T2 sequences and C1/C2 sequences) provides a general explanation for PTGS. A connectron can implemented by RNA sequences, PNA (Peptide Nucleic Acid) sequences or by a zinc-finger DNA Binding Protein (DBP) specific to the T1 and T2 sequences.

Characteristically the adjacent C1/C2 sequences lie in the 3'UTR of a gene. The T1 and T2 sequences do not lie within the translated region of any gene. These sequences "surround" one or more genes. There are, however, T1 and T2 sequence pairs that surround one or more C1/C2 sequences that are not 3'UTR to any gene. These are called "geneless connectrons". There may be promoter sequences that cause the transcription of these 3'UTR sequences.

A computer-based algorithm that is similar to the algorithm used in the US Patent 6,205,404 has been developed to determine the connectron structure of any genome. This algorithm determines the existence of all the connectrons in the genomic DNA. Connectrons exist in prokaryotes, archea, single-celled eukaryotes, multi-celled eukaryotes, plants and higher animals. Connectron relationships exist between prokaryotes and their plasmids. The geneless connectrons provide a possible mechanism for forming a hierarchy of gene expression control that will produce an understanding of cell differentiation and tissue development.

Each connectron is a unique tetrad of sequences. Each connectron changes the expression of the genes between the T1 and T2 sequences. The C1 sequence (which is equivalent to the T1 sequence) and the C2 sequence (which is equivalent to the T2 sequence) are determined by the invention described in this patent application. In general, the tetrad of connectron sequences can be patented because the structure of matter is known and the function of specific gene expression modulation is also known. Gene expression modification can be produced by introducing antisense

RNA or PNA to interact C1/C2 RNA sequences or zinc-finger DBPs to interact with the T1 and T2 sequences. Using connectrons it will be possible to modify cellular and tissue behavior in a very general manner.

Examples will be given from different genomes to illustrate that the connectron is a perfectly general and universal concept.

Definitions

Double stranded DNA – Watson and Crick showed in 1953 that DNA naturally forms a double-stranded helix. A typical double stranded sequence is

5'-TAGAGGAGTACCAC-3'
3'-ATCTCCTCATGGTG-5'

Hydrogen Bond - The force between a hydrogen atom and another heavier atom such as Oxygen (O), Nitrogen (N), Phosphorus (P), or Sulfur (S).

Positive strand – The positive strand is normally represented 5' to 3' running left to right as in

5'-TAGAGGAGTACCAC-3'

Negative strand – The negative strand is normally represented 5' to 3' running right to left as in

3'-ATCTCCTCATGGTG-5'

Single stranded RNA – Either the positive or the negative strand of the double-stranded DNA can be transcribed by the polymerase. In RNA U replaces T.

RNA of positive strand sequence	5'-UAGAGGAGUACCAC-3'
RNA of negative strand sequence	5'-GUGGUACUCCUCUA-3'

Antisense RNA – The antisense strand of any RNA sequence is the compliment sequence

RNA sequence	5'-UAGAGGAGUACCAC-3'
Antisense RNA sequence	3'-AUCUCCUCAUGGUG-5'

Triple Strand Helix – The RNA sequence of a RNA/DNA triple-strand complex is the same as the positive strand of the DNA

DNA positive strand	5'-TAGAGGAGTACCAC-3'
DNA negative strand	3'-ATCTCCTCATGGTG-5'
RNA strand	5'-UAGAGGAGUACCAC-3'

Promoter – Any region of DNA, that binds proteins which engage the polymerase transcription mechanism.

TATA Box – A region near the 3' end of a promoter with the sequence TATA.

mRNA – The RNA produced from the DNA by the polymerase as a result of transcription

Start of transcription – The 3' end of a promoter where the polymerase mechanism begins to transcribe DNA into mRNA.

Exon – Any region of mRNA which is used to code for proteins

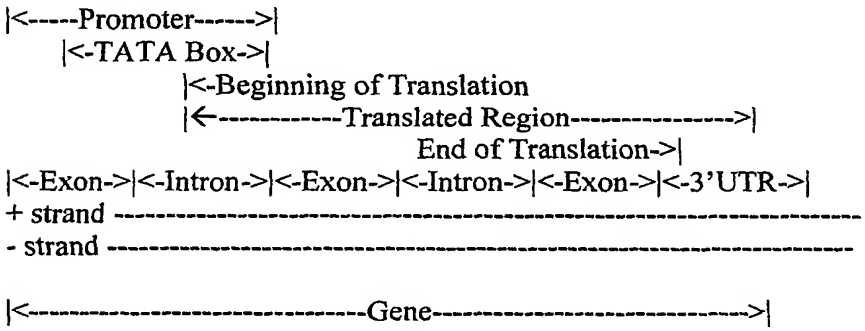
Intron – Any region of mRNA lying between two exons which is not used to code for proteins. The introns are edited out of the initial RNA transcript to form the mature mRNA.

3' UTR – The untranslated 3' end of an mRNA is beyond the end of the last exon. A stop codon in the mRNA causes the ribosome to stop the translation of mRNA into protein.

End of translation – The 3' end of the 3'-most exon.

Translated region – Any collection of exons and introns.

Gene – Any DNA region that codes for a protein. Introns do not occur in prokaryotic genes and they sometime fail to occur in eukaryotic genes. A typical model of a gene is



Positive strand gene – Any gene in which the features run 5' to 3' on the positive strand

Negative strand gene – Any gene in which the features run 5' to 3' on the negative strand

C1 sequence – Any positive or negative strand DNA sequence of 20 bases or more.

The C2 sequence must occur in the same chromosome as the C1 sequence.

C2 sequence – Any positive or negative strand DNA sequence of 20 bases or more. The C1 sequence must occur in the same chromosome as the C2 sequence.

C1/C2 – Any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence

T1 sequence – Any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence. The T1 and T2 sequences must be between about 1kb and 105kb apart.

T2 sequence – Any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence. The T2 and T1 sequences must be between about 1kb and 105kb apart.

Last exon gap or Gap-Distance – The number of bases between the end of transcription and the beginning of the C1/C2 sequence. In prokaryotes and single-celled eukaryotes this gap can range from no bases to 500 bases. In multi-celled eukaryotes the gap can be as large as 10,000 bases.

Poly-adenylation signal – A number of Adenosine (A) bases are added to the mRNA at the end of the 3'UTR.

Possible Connectron – Any set of T1, T2 and C1/C2 sequences such that the C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. The promoter of some gene causes the mRNA of the gene to be expressed. The mRNA is edited to eliminate the introns. The whole mRNA including the 3'UTR can move about in the cell or the nucleus of the cell. The C1/C2 RNA that is part of the 3'UTR moves to the T1 and T2 DNA sequences. A triple-stranded complex of the DNA and the RNA forms such that the C1 sequence forms hydrogen bonds with the T1 sequence and the C2 sequence forms hydrogen bonds with the T2 sequence.

Because the C1 sequence is adjacent to the C2 sequence, the T1 sequence is brought physically close to the T2 sequence. This produces a loop of between about 1kb and 105kb in the DNA. Histone proteins reduce the length of the DNA by binding 200 bases. Histone/DNA complexes form six-fold symmetry chromatin assemblies. The diameter of the chromatin assemblies is approximately 30nm.

Real Connectron – Any Possible Connectron which is within the Gap-Distance of some gene

Homologous connectron – The T1 sequence and the T2 sequence are on the same chromosome as the C1/C2 sequence

Heterologous connectron – The T1 sequence and the T2 sequence are on a chromosome different from chromosome of the C1/C2 sequence

Permanent connectron – Any C1/C2 sequence, which is 3' UTR to some gene that is not surrounded by any T1 and T2 sequence pairs

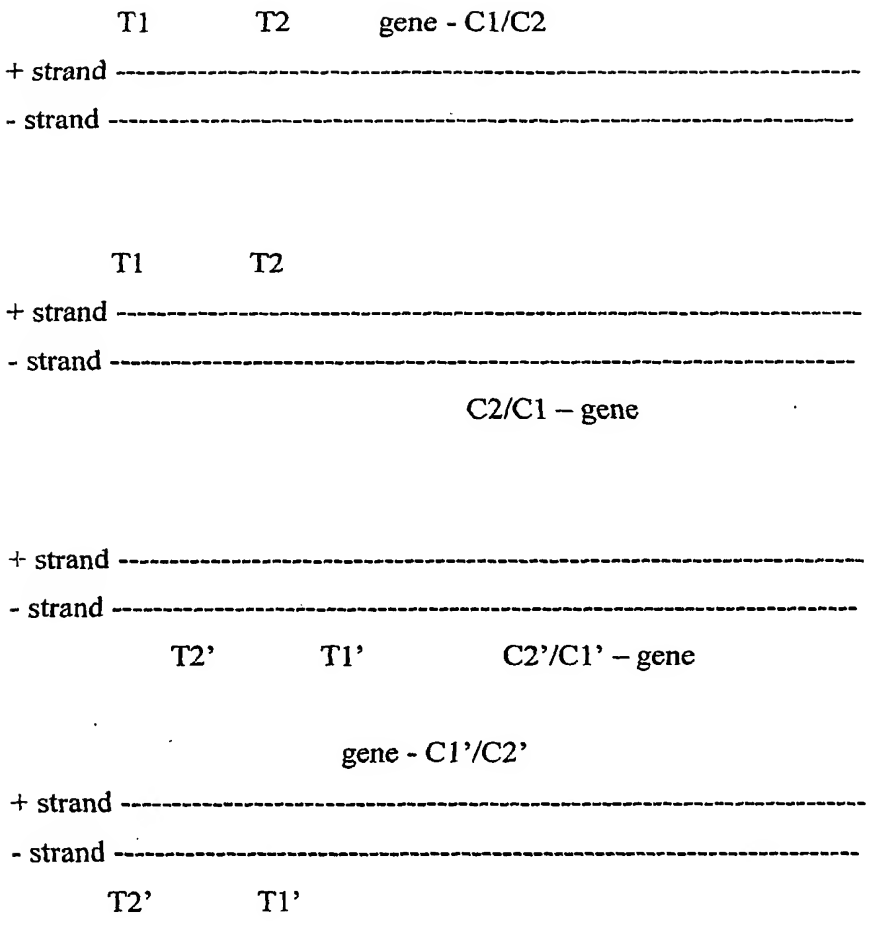
Transient connectron – Any C1/C2 sequence, which is 3' UTR to some gene that is surrounded by one or more T1 and T2 sequence pairs

Self-limiting connectron – Any C1/C2 sequence which is 3'UTR to some gene that is surrounded by the T1 and T2 sequences such that C1=T1 and C2=T2

Geneless connectron - Any C1/C2 sequence which is not 3'UTR to some gene but is surrounded by some T1 and T2. A promoter may lie 5' to the C1/C2 sequence.

Bidirectionality of Connectron Excitation – A C1/C2 short loop on one strand selects a T1-T2 long loop pair on the same or the opposite strand. The C1/C2 short loop has a complementary C1'/C2' sequence on the opposite strand. Similarly the T1-T2 long loop pair has a complementary long loop pair T1'-T2'. Wherever a C1/C2, T1-T2 tetrad exists there is a complementary C1'/C2', T1'-T2' tetrad. The C1/C2 short loop

can be transcribed as a 3'UTR to a gene on the same strand. The C1'/C2' short loop which is on the strand opposite to the C1/C2 short loop can also can be transcribed as a 3'UTR to a gene on the same strand. There are four possible models of action



Of course, the short loops and the long loops do not have to be on the same chromosome.

Hierarchy of connectron action – When a C1/C2 is expressed it forms a T1-T2 loop by forming a connectron. The C1/C2 sequence does not have to be on the same chromosome as the T1 and T2 sequences. This provides a way of causing interaction between chromosomes. When the T1-T2 loop forms, any genes in that loop region which had been expressing C1/C2 sequences in their 3'UTRs, now cease expressing the C1/C2 sequences. The connectrons formed by these C1/C2 sequences will cease to exist after some time thus opening up the genes inside the respective T1-T2 loops

to expression. The hierarchy of connectron action is alternates between repression and expression. The connectron hierarchies can be of any depth.

One-to-Many connectron action – One C1/C2 sequence can form connectrons in many different places on many different chromosomes. The only requirement is that C1=T1 and C2=T2. This makes it possible for one expression event to control the expression of many genes on different chromosomes.

Many-to-One connectron action – C1/C2s that come from many different places on many different chromosomes can form a connectron for a specific T1-T2 sequence pair. The only requirement is that C1=T1 and C2=T2. This makes it possible for many different expression events to control the expression of one set of genes on a particular chromosome.

Many-to-Many connectron action – The arrangement of C1/C2s and T1-T2s across chromosomes can form a complex web of gene expression control relationships.

Percentage of the Genome Regulated by Connectrons – Since the connectrons for a sequenced genome can be calculated, the percentage of the genome that is open to connectron regulation can be known.

Emergent Property – The network of connectrons in any genome emerges from a knowledge of the complete DNA sequence of the genome. Because both the C1/C2 sequences and the T1-T2 sequences can be any place in the genome, the whole genomic sequence must be known before all the connectrons can be determined.

Paradigm Shift – For the past fifty years since the discovery by Watson and Crick of the double-helical nature of DNA, the reigning paradigm for scientific discovery has been the study of one gene and its effects on the behavior of a cell. The advent of genomic sequencing and this invention of connectrons that emerge from the whole genome will produce a shift in the way scientists view biological systems and the way they formulate and execute experiments. The many-to-many relationships between

the connectrons means that there are many ways in which the expression of a set of genes can be modulated. The multiplicity of control pathways means produces a system stability that makes it possible for biological systems to be stable for long periods of evolutionary time. The thinking that goes into formulating scientific experiments will have to change to accommodate the changes in understanding that will be induced by the application and extension of this patent application.

Hierarchy of DNA Structuring – The DNA of a cell's genome is structured in a hierarchy of six levels. Figures 1, 2 and 3 have been adapted from The Molecular Biology of the Cell by Alberts, Bray, Lewis, Raff, Roberts and Watson [third edition pages 354, 345 and 348]. As shown in figure 1, the double stranded DNA is level 1. The double-stranded DNA is wrapped around histone proteins to form a chromatin particle that is level 2 of the hierarchy. Level 2 is described as "beads-on-a-string" in figure 1. The chromatin particles are packed in a six-fold symmetry as shown in figure 2a and figure 2b. These six-fold assemblies have a diameter of 30 nm. Each 30 nm assembly contains from 18 (i.e. 6 * 3) to 30 (i.e. 6 * 5) chromatin particles. The 30 nm assemblies aggregate into large loops which range in length from 5,000 bases to 100,000 bases of DNA. The size of these large loops as shown in figure 1 is approximately 300 nm. These large loops constitute level 4 of the structuring hierarchy. As shown in figure 1, level 5 of the DNA structuring hierarchy many large loops are condensed to form a structure which is approximately 700 nm in diameter. The complete chromosome that constitutes level 6 of the hierarchy is composed of two very long sections of level 5 DNA.

Model of Chromatin Structure – The level 4 structure of DNA as shown in figure 1 ranges in length from 5,000 to 105,000 bases of DNA. Figure 3 shows that proteins are thought to connect portions of the long loops formed by the 30 nm particles to form a chromosome axis. These condensed long loops are described as chromomeres in The Molecular Biology of the Cell.

Prior Art

The chromomere model of DNA structuring was presented by N. A Resnik, et al.[1] and is based on electron microscopic data. There are more recent papers studying a variety of genomes with electron microscopy but no equivalent study of chromomeres has been done on a fully sequenced genome.

A recent News Feature in Nature by T. Gura [2] described the discovery of post-transcriptional gene silencing in which viral RNA interacts with the transcribed RNA of the cell to silence the expression of genes. This article describes experiments in C. elegans and D. megalomaster in which RNA that is complementary to mRNA introduced into a cell. This "antisense" RNA has the effect of turning off the expression of one or more genes. The introduced complementary RNA produces an "RNA interference" called RNAi.

Thomas Werner and his colleagues at Genomatix in Munich, Germany have developed an approach to understanding what they call "Matrix Attachment Region" (MAR). Figure 5 shows their interpretation of the structure of DNA surrounding a gene. The following description of the MAR is copied from the Genomatrix web site

"Matrix Attachment Regions (MARs) MARs are sequence regions that are responsible for the attachment of genomic DNA to the nuclear matrix or scaffold. Transcription absolutely requires anchorage of genomic DNA to the nuclear matrix.

Functional features of MARs:

Anchoring of regulatory elements like promoters and enhancers to the nuclear matrix.

Ensuring long term activity of promoters and enhancers in chromatin.

Insulation, rendering a functional domain insensitive to position effects.

Genomatix is conducting a research project to define and detect MARs by computer-analysis."

Brief Description of the Objects of the Invention

An object of the invention is to provide a method of identifying DNA sequences that control the expression of different collections of genes in a genome comprising, detecting selected DNA sequences adjacent to some genes excluding exons and introns.

An object of the invention is to provide a method of identifying DNA sequences that control the expression of different collections of genes comprising, detecting, by computer, one or more pairs of non-adjacent DNA sequences to which are bound to two RNA sequences.

An object of the invention is to provide a method of identifying DNA sequences that control the expression of different collections of genes in a genome comprising detecting changes in connectron behavior in the genome.

An object of the invention is to provide a method of modifying the expression of different gene collections in a genome, comprising detecting changes in connectron behavior as a result of an exogenous stimulus.

An object of the invention is to provide a method of detecting where and when new genes are being integrated into a host genome comprising detecting the connectrons in said host genome.

An object of the invention is to provide a method of detecting the expression effect of different gene collections in a given body comprising detecting the back and forth flow of connectrons between the chromosomes thereof.

An object of the invention is to provide a method of modifying a given body comprising modifying the connectron organization therein.

An object of the invention is to provide a method of detecting connectron control and target sequences in a given genome comprising:

determining the base composition of said genome,
determining one or more sites of control sequence organization, and/or
determining one or more sites of target application.

An object of the invention is to provide a method of determining the response of a cell in any tissue to changes in the cell's environment and/or genetic composition comprising providing a complete genomic DNA sequence for the organism and determining the effect of changes in connectrons due to application of a given exogenous stimulus to the gnome.

An object of the invention is to provide a method of determining in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the tetradic relationship T1=C1 and T2=C2 where T1 and T2 are DNA sequences 20 or more bases in length, where the C1 sequence is adjacent to the C2 sequence, where the T1 and T2 sequences are on the same chromosome, and where the C1/C2 sequences are on the same chromosome as T1 and T2 or where the C1/C2 sequences are on a chromosome different from T1 and T2, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

An object of the invention is to provide a method of determining in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits many different C1/C2 short loops to control the existence of a T1-T2 long loop and wherein said C1/C2 short lops can be on the same chromosome or on different chromosomes from the T1-T2 long loop, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

An object of the invention is to provide a method of determining in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of many T1-T2 long loops, the C1/C2 short loop can be on the same chromosome or on different chromosomes from the T1-T2 long loops, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

An object of the invention is to provide a method of determining in the connectron relationships between prokaryotes and their plasmids wherein said connectrons implement a control mechanism between the two genomes that makes it possible from

them to form a symbiotic relationship, and in the case of D. radiodurans the relationship is not symmetric, and the D. radiodurans genome sends C1/C2 short loops to the MP1 plasmid, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

An object of the invention is to provide a method of determining that connectron relationships that exist in plant and higher animals.

An object of the invention is to provide a method of determining in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of one or more T1-T2 long loops without being subject to any expression controls other than those of the gene to which the C1/C2 is 3'UTR, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 540 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart,

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart, and

3'UTR - untranslated 3' end of an mRNA is beyond the end of the last exon, a stop codon in the mRNA causes the ribosome to stop the translation of mRNA into protein.

An object of the invention is to provide a method of determining in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of one or more T1-T2 long loops such that this C1/C2 short loop is itself subject to expression control by another T1-T2 long loop which surrounds it, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 540 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

An object of the invention is to provide a method of determining in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of the T1-T2 long loop that surrounds it, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

An object of the invention is to provide a method of determining the connectron relationships that do not have any genes within the T1-T2 long loop, wherein:

T1 sequence is any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, and the T2 or T1 sequences must be between about 1kb and 105kb apart.

An object of the invention is to provide a method of determining the geneless connectron relationship where one C1/C2 short loop controls the existence of many geneless T1-T2 long loops, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

Description of the Drawings and Tables

The above and other objects, advantages and features of the invention will become more apparent when considered with the following specification and accompanying drawings and tables wherein:

Figure 1 DNA is structured in six levels of increasing condensation. Double stranded DNA is level 1. Two turns of DNA are wrapped about each chromatin particle at level 2. The chromatin particles which each containing 200 base pairs form into 30 nm particles at level 3. The 30 nm particles form into large loops with an approximate dimension of 300 nm at level 4. Metaphase chromosomes form a condensed structure with an approximate dimension of 700 nm at level 5. An entire metaphase chromosome has a width of approximately 1400 nm at level 6. The large loops at level 4 of the DNA structuring are thought to have between 20,000 (20 kb) and 100,000 (100 kb) base pairs.

The Molecular Biology of the Cell by Alberts, Bray, Lewis, Raff, Roberts and Watson, 3rd. ed. , Garland Publishing, Inc., New York, 1994, p. 354

Figure 2 (a) Chromatin DNA forms into a six-fold symmetry 30nm particles.

(b) The six-fold symmetry 30nm particles form a linear chain with a varying number of repeat units.

The Molecular Biology of the Cell by Alberts, Bray, Lewis, Raff, Roberts and Watson , 3rd. ed. , Garland Publishing, Inc., New York, 1994, p. 345

Figure 3 Long loops of 30nm particles are thought to be closed at the bottom of the loop by proteins.

The Molecular Biology of the Cell by Alberts, Bray, Lewis, Raff, Roberts and Watson, 3rd. ed. , Garland Publishing, Inc., New York, 1994, p. 348

Figure 4 (a) Transcription and Editing. (b) Movement of the RNA through the Nucleus. (c) Connectron Formation

Figure 5 Overview of schematic organization of a typical transcriptionally active chromosomal loop.
From http://genomatix.gsf.de/func_genomics/functional_genomics.html

Table 1 Connectron Properties for Prokaryotic, Archea and Eukaryotic Genomes

Table 2 Yeast Inter-Chromosomal Connectron Distribution

Figure 6 Genome size plotted as a log-log function of the Number of Connectrons

Figure 7 Number of Sequence Instances plotted as a function of the Number of Fragments

Figure 8 Level 0 – The overall view of the algorithm

Figure 9 Level 1 – Process Flow of the Algorithm

Figure 10 Level 2a – two pages – Process Genome into Blocking Fragment File

Figure 11 Level 2b – two pages – Compute the Connectrons for a Genome

Figure 12 Level 2c – two pages – Analyze Possible Connectrons

Figure 13 Level 3a – Setup Genome Usage Memory

Figure 14 Level 3b – Find DBP-Size Blocking File for T1-Window

Figure 15 Level 1 – Find DBP-Size Blocking File for T2-Window

Figure 16 Level 2a – two pages – Find C1/C2 Entries

Figure 17 Level 2b – two pages – Scan Genome Usage Memory for Potential Connectrons

Description of the Invention

A connectron is a relationship among four DNA sequences. Each sequence must be at least 20 bases long. There is a report by Sharp and Zamore [3] that RNA sequences of "about length 25" are important as sources of RNAi. 27 bases were actually used as the minimum length of each of the sequences. The T1 sequence is on one strand of some chromosome in a genome. The T2 sequence is on the same strand of the same chromosome as the T1 sequence. The T1 and T2 sequences (which are each at least 20 bases in length) must be at least 5,000 bases distant from each other but they can not be more than 105,000 bases distant from each other. The C1 sequence and the C2 sequence (which are each at least 20 bases in length) are adjacent to each other on some strand of some chromosome in the genome. The C1/C2 sequences – called the "short loop" – can be on the same strand as the T1 and T2 sequences or they can be on the opposite strand. The C1/C2 sequences of the short loop can be on the same chromosome as the T1 and T2 sequences but they can also be on a different chromosome in the genome. When a genome has only one chromosome, then the point is moot. Many genomes, of course, have several chromosomes. The C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence.

The C1/C2 sequence must be on the same strand as a gene, either be directly adjacent to the gene (i.e. a gap of 0 bases) for prokaryotic genomes or at this time be within 10,000 bases for eukaryotic genomes. The size of the gap between the end of the gene and the beginning of the C1/C2 sequence is a variable. The C1/C2 short loop is expressed as the 3'UTR (Un-Translated Region) of the gene. In the case of prokaryotic genes that do not normally have introns, the whole mRNA becomes the active species for connectron formation. In the case of eukaryotic genes, the whole transcript is the active species for connectron formation upon editing of the transcript to eliminate the introns. The whole transcript then can move about in the cytoplasm of prokaryotic cells or the nucleus of eukaryotic cells. Since the C1 sequence is equivalent to the T1 sequence and the C2 sequence is equivalent to the T2 sequence,

the C1 RNA can form a Hoogsteen triple-stranded RNA/DNA/DNA helix with the double-stranded T1 sequence. Similarly the C2 RNA can form a Hoogsteen triple-stranded RNA/DNA/DNA helix with the double-stranded T2 sequence. Because the C1 sequence and the C2 sequence are adjacent to each other, the C1/T2 RNA/DNA/DNA Hoogsteen triple helix is brought into physical adjacency to the C2/T2 RNA/DNA/DNA Hoogsteen triple helix. RNA/DNA/DNA hybrid helices are the most stable form of triple helix. RNA double helices, DNA double helices, RNA triple helices and DNA triple helices are all significantly less stable than a RNA/double-stranded DNA triple helix. The stable physical adjacency of the two triple-stranded Hoogsteen helices ensures that the long loop of double-stranded DNA between the T1 sequence and the T2 sequence can then be structured into 30 nm chromatin particles as shown in level 4 of figure 1. The genes on either strand of the DNA between the T1 sequence and the T2 sequence when they are structured into the 30 nm chromatin particles are not open to promotion and expression.

The tetradic relationship between the T1 and T2 sequences that form the long loop and the C1/C2 sequences that form the short loop are called a connectron. The name "connectron" was suggested by J. David Rawn Ph.D. of Towson University. A connectron is possible if the T1, T2, C1 and C2 sequences exist. A connectron is real if the C1/C2 short loop sequence is adjacent to an expressible gene. If the expression of the adjacent gene is inside one or more T1 – T2 long loops then this connectron is said to be transient. If the adjacent gene is not inside any possible T1-T2 long loop then the connectron is said to be permanent. If a connectron is inside of a T1-T2 long loop that has the same sequences (i.e. T1 is really equal to C1 and T2 is really equal to C2) then the connectron is said to be self-limiting. This is true because once the C1/C2 sequence is expressed it forms the T1-T2 long loop that then shuts off the expression of the gene adjacent to the C1/C2 sequence. Self-limiting conectrons can also be called "spike" connectrons since they generate a short-duration spike of the C1/C2 short loop sequence. If a T1-T2 long loop does not contain any genes but it contains C1/C2 short loop sequences then this type of connectrons is said to be geneless. The C1/C2 short loops within a geneless T1-T2 long loop can, of course, control the expression of genes.

The physical existence and lifetimes of the connectrons must be proved by molecular biological experimentation. This physical experimental process, however, is logically quite separate from the computational experimentation that have been conducted from June of 1999 to May of 2001. The computational search for the existence of connectrons has been extremely positive. These computations have shown that connectrons exist in prokaryotes, in archea, between prokaryotes and their plasmids, in single-celled eukaryotes, in multi-celled eukaryotes, in plants, in higher animals and in humans. All of these features and properties are described in the claims section that follows.

The connectron invention is very powerful. It depends only on sequence equivalency. The minimum length of the four sequences seems to be about 20 bases. In the calculations shown in this patent application, 27 bases have been used as a minimum. The Nature News Feature [1] says that other scientists have found RNA sequences of length about 25 that have interesting gene silencing properties. The Nature article does not give any mechanism. Because of my algorithm and its use on a variety of genomes, this patent application provides the computational proof that a particular mechanism is highly probable. The connectron invention provides an explanation for how communication occurs with a chromosome as well as between chromosomes in genomes that have more than one chromosome. Since each T1-T2 long loop can contain one or more genes, the connectron invention provides a mechanism for turning on and turning off sets of genes simultaneously. In time, the connectron invention will provide an explanation for how differentiation of how one cell's behavior differs from the behavior of another adjacent cell. It is already clear from the computational experiments that have been made on S. cervesiae, C. elegans and D. megalomaster that the number of geneless connectrons increases dramatically as evolution proceeds from single-celled eukaryotes (i.e. S. cervesiae) to 1,000 cell eukaryotes (i.e. C. elegans) to visible creatures (i.e. D. megalomaster). The extension of this evolutionary progress to plants (i.e. A. thaliania) for which only three chromosomes are sequenced and humans (i.e. H. sapiens) for which only one chromosome is completely sequenced. Although the complete human genome was

published in Nature and Science in February of 2001, the NIH-sponsored genomic sequencing results are available for about 1/3 of the bases in the whole genome. The human genomic sequence determined by Celera Genomics, Inc. is available only by subscription. Table 1 shows how the genome size, the number of gene-containing and geneless connectrons and the percentage of genes controlled are related in many different genomes.

The C1/C2 short loops originate on one chromosome. The T1-T2 long loops can be on the same or different chromosomes. Table 2 which is for yeast (S. cervesiae) is a square matrix of how many C1/C2 short loops on a given chromosome are sent to form T1-T2 long loops on other chromosomes. The diagonal of this matrix shows that many chromosomes send connectrons to themselves. The striking feature of this particular table is that chromosome 6 only sends connectrons to chromosome 12 but that it receives connectrons from chromosomes 4,5,7,10,12,13,15 and 16.

Any tetrad of connectron sequences (i.e. the T1, T2, C1 and C2 sequences) as well as the fact of the adjacency of the C1/C2 short loop sequence to the transcribing gene can be patented because the content of matter and the utility can be exactly described. The utility of a connectron is that the T1-T2 long loop shuts off the expression of the genes that lie between the T1 sequence and the T2 sequence. In the case of geneless connectrons, the utility is of a higher level in that the C1/C2 short loops contained in the higher-level geneless T1-T2 long loop, eventually form other lower-level T1-T2 long loops around a set of genes.

The invention of connectrons comes at a particularly important time in biological discovery. The geneless connectrons make a many-to-many hierarchical control mechanism possible. It is already clear from the determination of the conectrons for C. elegans and D. megalomaster that there are as many or more geneless connectrons than there are genes. It has been clear for some time that the number of genes in a genome is not particularly correlated with the size of the genome. Figure 6 shows that the size of a genome is roughly linearly correlated with the number of connectrons.

The connectron invention can be used to generate a model of behavior in any cell. The simulation of connectron behavior in different genomes will be the subject of another patent application.

5

The connectron invention provides for a rational exploitation of the information contained in the raw genomic DNA sequence by forming a hierarchy of relationships between geneless connectrons, transient connectrons, permanent connectrons, self-limiting connectrons and the expression of genes.

10

Detailed Description of the Invention

The algorithm for the determination of connectrons in any genome or any genome fragment is represented in the following flow diagrams. The Level 0 diagram in figure 8 shows the general relationships in a digital computer. The central processor of the digital computer uses the computer program to take genome descriptors, the genomic DNA sequences and the tables of gene features to produce a file of blocking fragments and a file of the optimal connectrons for the genome. The printer serves to make hard copies of the files and this patent application. The level 1 diagram in figure 9 shows the three essential steps in the determination of connectrons. The genome is first processed into a blocking fragment file. Then the blocking fragments are used to compute the connectrons for the genome. Finally the potential connectrons are analyzed to determine if the C1/C2 sequences are in the 3'UTR of a gene. The level 2a diagram in figure 10 shows the steps required for the processing of the genome into a file of blocking fragments. The genomic DNA sequence is decomposed into 27-base frames for both the positive and negative strands. These fragments are written to the unsorted fragment file. The fragment file is then sorted is then read and formed into groups of equivalent sequences. The (.blk) file contains the sequence and a pointer to the (.gptr) file which contains the pointers to the position of the fragments in the genomes. The position in the genome includes the chromosome number, the position in the chromosome and the strand (i.e. positive and negative). A sample of these files follows

Sample of the (.blk) file for S. cervesiae

27-base fragment	Number of instances	Pointer to (.gptr) file
111111111111111111111111111	0	1
111111232442333133324434l4	1	2
111111141113443133314333341	2	4
111111232442333133324434141	1	5
111111323311133323144423444	2	7
111111332213331341414443413	2	9
111111333444112343412323243	1	10

111111333444113343412323243	9	19
111111411134431333143333414	2	21
111111443223134142124434124	2	23
111112223234344444443144442	2	25
111112244123441122214421213	8	33
111112311241114344334134431	2	35
111112324423331333244341414	1	36
111112344232231344242234342	1	37
111112433444244421144134211	1	38
111112444311313442332142224	1	39
111113131241131114424413231	1	40
111113143332344311113133411	1	41
111113233111333231444234441	2	43

In fragments above 1=G, 2=C, 3=A, 4=T

Sample of the (.gptr) file for S. cervesiae

There are 16 chromosomes in S. cervesiae

Item	Chromosome	Position in Chromosome	Direction
1	0	0	0
2	4	11137	1
3	12	467619	1
4	12	458482	1
5	4	11138	1
6	12	465759	2
7	12	456622	1
8	1	219366	1
9	8	539978	1
10	14	522451	1
11	4	1099073	1
12	4	1210003	1
13	7	539068	1
14	12	654136	1
15	12	596455	1
16	15	121016	1
17	15	598127	2
18	16	847724	1
19	16	59765	1
20	12	467620	1
21	12	458483	1
22	12	461657	1
23	12	452520	1
24	13	838006	1

25	15	288270	1
26	4	83593	1
27	4	992867	1
28	6	162265	1
29	7	845687	1
30	10	531560	2
31	15	282208	1
32	16	860418	1
33	16	572308	1
34	12	465992	1
35	12	456855	1
36	4	11139	1
37	8	89343	1
38	4	10302	1
39	1	19894	2
40	16	9311	1
41	10	735203	1
42	12	465760	1
43	12	456623	1

In direction column above 1=positive strand, 2=negative strand

The level 2b diagram in figure 11 shows the computation of the connectrons. The genome descriptors consist of the number and length of the chromosomes. The algorithm uses an array that represents several facts about each base position in the genome. The level 3a diagram in figure 13 shows the setup of the Genome-Usage memory. The gene features are used to prevent the region of the genome that codes for proteins from being used for the connectron sequences (i.e. the T1s, the T2s, the C1s and the C2s). In the level 2a diagram of figure 10, the algorithm steps through each chromosome and within each chromosome through each base position looking for acceptable T1-windows of 27 bases. A T1-window can be used to form a connectron relationship if there are two or more instances of this fragment in the blocking fragment file. The computation in the level 3b diagram of figure 14 determines if the T1-window is acceptable of not. Once an acceptable T1-window is found, the algorithm (in the level 2a diagram of figure 10) looks for acceptable T2-window positions that lie between 5,000 and 105,000 bases from the T1-window. The computation for determining acceptable T2-window positions is done in the level 3c diagram of figure 15. Once a pair of T1 and T2 window positions are found, the

algorithm looks among the instances of these T1 and T2 sequences for a pair of sequences C1 and C2 that lie within 200 bases of each other on the same chromosome. The computation for determining acceptable C1/C2 windows is shown in the level 3d diagram in figure 16. In the level 3e diagram of figure 17 the Genome-Usage memory is scanned for the Possible-Connectrons. In the level 2c diagram of figure 12 the Possible-Connectrons are scanned to determine if the C1/C2 sequences are within the Gap-Distance of a gene on either the positive or the negative strands. The Real-Connectrons are then written out in several different files including the descriptions in the claims section.

Examples

The algorithm for the determination of optimal connectrons has been applied to a number of different publicly available genomes. The connectron is a tetradic relationship between four sequence elements – T1, T2, C1 and C2. The claims presented in this section are written by the program NearGene that implements the flow diagram Level 2c of figure 12. The examples are written a uniform type of English. Each example contains some or all of the following elements

---

Name of genome
Description of T1
Length of T1-T2 loop
The chromosome on which the T1-T2 loop exists
The identifier number within the genome of the T1 sequence
The T1 sequence
Description of T2
The identifier number within the genome of the T2 sequence
The T2 sequence
A list of genes whose expression is controlled by the T1-T2 loop
The common names of the genes as obtained from the NCBI gene feature file (.ptt)
A list of C1/C2 short loops whose expression if controlled by the T1-T2 loop
The chromosome on which the C1/C2 short loop exists
The common name of the gene which expresses the C1/C2 short loop as an RNA
The sequence of the C1/C2 short loop
A list of C1/C2 short loops that control the formation of the T1-T2 loop
The chromosome on which the C1/C2 short loop exists
The common name of the gene which expresses the C1/C2 short loop as an RNA
The sequence of the C1/C2 short loop

The match between the C1/C2 sequence and the T1 sequence
The match between the C1/C2 sequence and the T2 sequence

The uniform descriptions make it possible to rapidly comprehend the specifics in each example.

When a sequence element is very long a series of four dots has been inserted between the beginning and ending sequence groups. A variable number of bases have been deleted.

Index of Pages for Connectron Samples

Page 164

9. Geneless connectrons exist in single-celled and multi-celled eukaryotes

Page 174

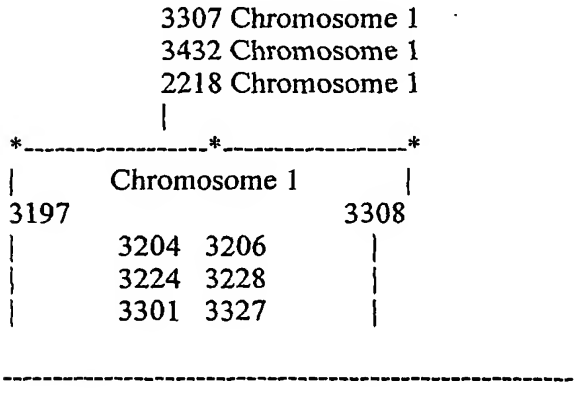
10. One connectron controls many geneless connectrons in single-celled and multi-celled eukaryotes

1. Connectrons occur in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

Connectrons exist as tetradic relationships where the sequence T1 is equivalent to the sequence C1 (written T1=C1) and where the sequence T2 equals the sequence C2 (written T2=C2) where T1 and T2 are DNA sequences 20 or more bases in length, where the C1 sequence is adjacent to the C2 sequence, where the T1 and T2 sequences are on the same chromosome, and where the C1/C2 sequences are on the same chromosome as T1 and T2 or where the C1/C2 sequences are on a chromosome different from T1 and T2. The connectron relationship has been found to exist in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

Example of a prokaryote connectron – E. coli

In this example the existence of the T1-T2 (3197-3308) long loop is controlled by three C1/C2 short loops (3307, 3432 and 2218). The T1-T2 long loop controls the expression of 64 genes on chromosome 1 in addition to six C1/C2 (3204, 3206, 3223, 3228, 3301 and 3327) short loops. The C1/C2 short loop 3327 lies outside the range of the T1-T2 long loop (3197-3308) but this C1/C2 is expressed as a 3'UTR to the gene hemG that is within the range of the T1-T2 long loop.



Connectron control elements for chromosome 1 of the E. coli genome

A double stranded DNA loop of length 93.542 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3197. This T1 control element has the DNA sequence

AAAAAATGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGG
AATAACTCCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACG
CCGCCGGGTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAA
ATAAATGCTTGACTCTGTAGCGGGAA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3308. This T2 control element has the DNA sequence

TAAATTTCCTCTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTG
ACACGGAACAACGGCAAACACGCCGCCGGGTCAGCGGGGTTCTCCTGAG
AACTCCGGCAGAGAAAGCAAAAATAAATGCTTGACTCTGTAGCGGGAAG
GCGTATTATGCACACCCCGCGCCGCT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

rrsC	gltU	rrlC	rrfC	aspT	trpT	yifA	yifE	yifB
ilvL	ilvG_1	ilvM	ilvE	ilvD	ilvA	ilvY	ilvC	ppiC
b3776	rep	gppA	rhlB	trxA	rhoL	rho	rfe	wzzE
wecB	rffH	wecD	wecE	wzxE	yifM_2	wecG	yifK	
argX	hisR	leuT	proM	aslB	aslA	hemY	hemX	
hemD	cyaA	cyaY	b3808	dapF	uvrD	b3814	corA	
yigF	yigG	rarD	yigI	pldA	recQ	yigJ	yigK	pldB
yigL	yigM	metR	metE	ysgA	udp	yigN	ubiE	yigP

b3836 yigU yigW_1 rfaH yigC ubiB fadA fadB pepQ trkH hemG

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 3204 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrsC and has the DNA sequence

GATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGG
CGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAG
ACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATG
GGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAA

A C1/C2 short loop on chromosome 1 whose identifier is 3206 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrsC and has the DNA sequence

GTCCCCTTCGTCTAGAGGCCCAGGACACCGCCCTTTCACGGCGGTAACAG
GGGTTCGAATCCCCTAGGGGACGCCACTTGCTGGTTTGTGAGTGAAAGTC
ACCTGCCTTAATATCTCAAAACTCATCTTCGGGTGATGTTTGAGATATTTG
CTCTTTAAAAATCTGGATCAAGCTGAAAATTGAAA

A C1/C2 short loop on chromosome 1 whose identifier is 3223 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrlC and has the DNA sequence

GCTGAAGTAGGTCCCAAGGGTATGGCTGTTCGCCATTTAAAGTGGTACGC
GAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGTCCCTATCTGCCGTGGG
CGCTGGAGAACTGAGGGGGGCTGCTCCTAGTACGAGAGGACCGGAGTGG
ACGCATCACTGGTGTTCGGGTTGTCATGCCAATGGCA

A C1/C2 short loop on chromosome 1 whose identifier is 3225 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrlC and has the DNA sequence

AAACAGAATTTGCCTGGCGGCCGTAGCGCGGTGGTCCCACCTGACCCCAT
GCCGAACTCAGAAGTGAAACGCCGTAGCGCCGATGGTAGTGTGGGGTCTC
CCCATGCGAGAGTAGGGAACTGCCAGGCATCAAATTAAGCAGTA

A C1/C2 short loop on chromosome 1 whose identifier is 3228 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrfC and has the DNA sequence

GGTCATAAAACCGGTGGTTGTAAAAGAATTCGGTGGAGCGGTAGTTCAGT
CGGTTAGAATACCTGCCTGTCACGCAGGGGGTCGCGGGTTCGAGTCCCGT
CCGTTCCGCCAC

A C1/C2 short loop on chromosome 1 whose identifier is 3301 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ubiB and has the DNA sequence

TTATCGTGCCTACAAATAGTCCGAACCGTAGGCCGGATAAGGCGTTTACG
CCGCATC

A C1/C2 short loop on chromosome 1 whose identifier is 3307 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene fadA and has the DNA sequence

TGCCGGATGCGGCGTAAACGCCTTATCCGGCCTACGGTTCGGACTATTTGT
AGGCA

A C1/C2 short loop on chromosome 1 whose identifier is 3327 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene hemG and has the DNA sequence

AAAAAATGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGG
AATAACTCCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACG
CCGCCGGGTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAA
ATAAATGCTTGACTCTGTAGCGGGAAGGCGTATTATG...CCCGTCACACCA
TGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCT
TACCACTTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTA
GGGGAACCTGCGGTTGGATCACCTCCTTACCTTAAAGAAGCGTTCTTTG

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 3307 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene hemG and has the DNA sequence

AAAAAATGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGG
AATAACTCCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACG
CCGCCGGGTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAA
ATAAATGCTTGACTCTGTAGCGGGAAGGCGTATTATG...CCCGTCACACCA

TGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCT
TACCACTTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTA
GGGGAACCTGCGGTTGGATCACCTCCTTACCTTAAAGAAGCGTTCTTTG

The match between the T1 sequence and the C1/C2 sequence is

AAAAAATGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGG
AATAACTCCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACG
CCGCCGGGTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAA
ATAAATGCTTGACTCTGTAGCGGGAA

The match between the T2 sequence and the C1/C2 sequence is

TAAATTTCCTCTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTG
ACACGGAACAACGGCAAACACGCCGCCGGGTCAGCGGGGTTCTCCTGAG
AACTCCGGCAGAGAAAGCAAAAATAAATGCTTGACTCTGTAGCGGGAAG
GCGTATTATGCACACCCCGCGCCGCT

A C1/C2 short loop on chromosome 1 whose identifier is 3432 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene btuB and has the DNA sequence

TGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGGAATAACT
CCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACGCCGCCGG
GTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAAATAAATG
CTTGACTCTGTAGCGGGAAGGCGTATTATGCACACC...ACACCATGGGAGT
GGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACT
TTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTAGGGGAAC
CTGCGGTTGGATCACCTCCTTACCTTAAAGAAGCGT

The match between the T1 sequence and the C1/C2 sequence is

TGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGGAATAACT
CCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACGCCGCCGG
GTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAAATAAATG
CTTGACTCTGTAGCGGGAA

The match between the T2 sequence and the C1/C2 sequence is

TAAATTTCCTCTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTG
ACACGGAACAACGGCAAACACGCCGCCGGGTCAGCGGGGTTCTCCTGAG
AACTCCGGCAGAGAAAGCAAAAATAAATGCTTGACTCTGTAGCGGGAAG
GCGTATTATGCACACCCCGCGCCGCT

A C1/C2 short loop on chromosome 1 whose identifier is 2218 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene clpB and has the DNA sequence

CTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTGACACGGAAC
AACGGCAAACACGCCGCCGGGC

The match between the T1 sequence and the C1/C2 sequence is

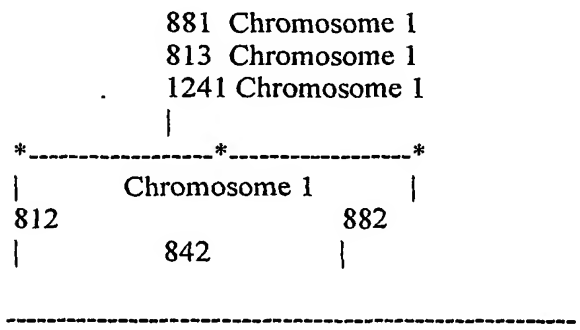
CTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTGACACGGAAC
AACGGCAAACACGCCGCCGGGC

The match between the T2 sequence and the C1/C2 sequence is

CTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTGACACGGAAC
AACGGCAAACACGCCGCCGGGTC

Example of an archea connectron – H. pylori

In this example the existence of the T1-T2 (812-882) long loop is controlled by three C1/C2 short loops (881, 813 and 1214). The T1-T2 long loop controls the expression of 54 genes on chromosome 1 in addition to one C1/C2 (843) short loop.



Connectron control elements for chromosome 1 of H. pylori genome

A double stranded DNA loop of length 96.385 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 812. This T1 control element has the DNA sequence

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 882. This T2 control element has the DNA sequence

TAGCGGAACTAAAGCATTCATCCCAAACACTAAAGATATTTGG

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

HP0999	HP1000	HP1001	HP1002	HP1003	HP1005	HP1006
HP1008	HP1009	HPtRNA-Pro	HP1010	HP1011	HP1013	HP1015
HP1017	HP1018	HP1020	HP1021	HP1022	HP1023	HP1024

HP1025	HP1027	HP1028	HP1030	HP1031	HP1033	HP1034
HP1038	HP1039	HP1040	HP1041	HP1042	HP1043	HP1044
HP1045	HP1046	HP1051	HP1052	HP1055	HP1056	HP1058
HP1060	HP1065	HPtRNA-Ser	HP1066	HP1067	HP1069	HP1070
HP1074	HP1075	HP1076	HP1077	HP1078	HP1079	HP1080
HP1081	HP1083	HP1084	HP1085	HP1088	HP1091	HP1092
HP1093	HP1094	HP1095	HP1096			

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 813 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene HP0998 and has the DNA sequence

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCATTCATCCC AAACACTAAAGATATTTGG

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 881 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene HP1096 and has the DNA sequence

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCATTCATCCC AAACACTAAAGATATTTGG

The match between the T1 sequence and the C1/C2 sequence is

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCA

The match between the T2 sequence and the C1/C2 sequence is

TAGCGGAACTAAAGCATTCATCCCAAACACTAAAGATATTTGG

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 813 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene HP0998 and has the DNA sequence

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCATTCATCCC
AAACACTAAAGATATTTGG

A C1/C2 short loop on chromosome 1 whose identifier is 881 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene HP1096 and has the DNA sequence

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCATTCATCCC
AAACACTAAAGATATTTGG

The match between the T1 sequence and the C1/C2 sequence is

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCA

The match between the T2 sequence and the C1/C2 sequence is

TAGCGGAACTAAAGCATTCATCCCAAACACTAAAGATATTTGG

A C1/C2 short loop on chromosome 1 whose identifier is 1241 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene HP1535 and has the DNA sequence

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCATTCATCCC AAACA

The match between the T1 sequence and the C1/C2 sequence is

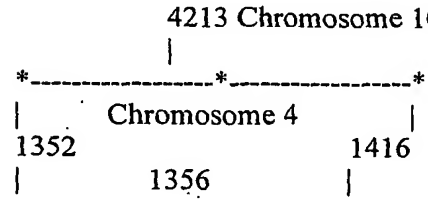
TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCA

The match between the T2 sequence and the C1/C2 sequence is

TAGCGGAACTAAAGCATTCATCCCAAACA

Example of single-celled connectron – S. cervesiae

In this example the existence of the T1-T2 (1352-1416) long loop on chromosome 4 is controlled by one C1/C2 short loop (4213) on chromosome 10. The T1-T2 long loop controls the expression of 34 genes on chromosome 4 in addition to one C1/C2 (1356) short loop.



Connectron control elements for chromosome 1 of S. cervesiae genome

A double stranded DNA loop of length 68.908 kilo-bases on chromosome 4 is bounded on the left by a T1 sequence whose identifier is 1352. This T1 control element has the DNA sequence

TTATGAGAAGCTGTCATCGAAGTTAGAGGAAGCTGAA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1416. This T2 control element has the DNA sequence

ATTAGATCTATTACATTATGGGTGGTATGTTGGAATAAAAATCAACTATCA
TCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGGTGTTAGA
AGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCTGAA
ACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAACATATAAAAC
GATGATAATAATATTTATAGAATTGTGTAGAATTGCAGATTCCCTTTTATG
GATTCCTAAATCCTTGAGGAGAACTTCTAGTATATCTACATACCTAATATT
ATAGCCTTAATCACAATGGAATCCCAACAATTACATCAAAATCCACATTC
TCTACAGTA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

YDR170W-A YDR171W YDR172W YDR173C YDR174W YDR175C
YDR176W YDR177W YDR178W YDR179C YDR179W-A YDR180W
YDR181C YDR182W YDR183W YDR184C YDR185C YDR186C
YDR187C YDR188W YDR189W YDR190C YDR191W YDR192C
YDR193W YDR194C YDR195W YDR196C YDR197W YDR198C
YDR199W YDR200C YDR201W YDR202C YDR203W YDR204W
YDR205W YDR206W YDR207C YDR208W YDR209C YDR210W

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 4 whose identifier is 1356 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YDR170W-A and has the DNA sequence

AATCACACTAATCATTCTGATGATGAACTCCCTGGACACCTCCTTCTCGAT
TCAGGAGCATCACGAACCCTTATAAGATCTGCTCATCACATACACTCAGC
ATCATCTAATCCTGACATAAACGTAGTTGATGCTCAAAAAAGAAATATAC
CAATTAACGCTATTGGTGACCTACAATTTCACTTCCAGGACAACACCAAA
ACATCAATAAAGGTATTGCACACTCCTAACATAGCCTATGACTTACTCAGT
TTGAATGAATTGGCTGCAGTAGATATCACAGCATGCTTTACCAAAAACGT
CTTAGAACG

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 10 whose identifier is 4213 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YJR029W and has the DNA sequence

ATCTATTACATTATGGGTGGTATGTTGGAATAAAAATCCACTATCGTCTAT
CAACTAATAGTTATATTATCAATATATTATCATATACGGTGTTAAGATGAT
GACATAAGTTATGAGAAGCTGTCATCGAAGTTAGAGGAAGCTGAAACGC
AAGGATTGATAATGTAATAGGATCAATGAATATAAACATATAAAACGGA
ATGAGGAATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGA
GGATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTAATA
TTATAGCCTTTATCAACAATGGAATCCCAACAATTATCTCAACAT

The match between the T1 sequence and the C1/C2 sequence is

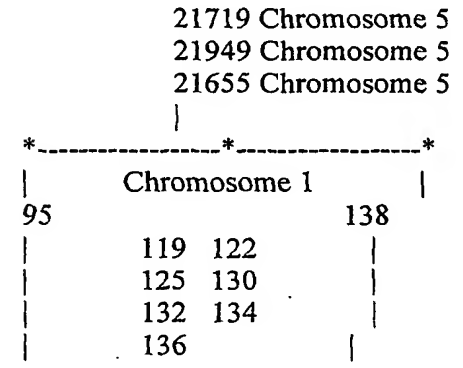
TTATGAGAAGCTGTCATCGAAGTTAGAGGAAGCTGAA

The match between the T2 sequence and the C1/C2 sequence is

ATCTATTACATTATGGGTGGTATGTTGGAATAAAAATC

Example of a multi-celled connectron – C. elegans

In this example the existence of the T1-T2 (9-138) long loop on chromosome 1 is controlled by three C1/C2 short loops on chromosome 5 (21719, 21949 and 21655). The T1-T2 long loop controls the expression of four genes on chromosome 1 in addition to seven C1/C2 (119, 122, 125, 130, 132, 134 and 136) short loops.



A double stranded DNA loop of length 41.978 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 95. This T1 control element has the DNA sequence

CAGCACGTTCTTAACCATGCAAAATCAGTTGAGAACTCTGCGTCTCTTCTC
CCGC

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 138. This T2 control element has the DNA sequence

ACTCTGCGTCTCTTCTCCCGCATTTTTTGTAGATCA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

Y73A3A.1 Y73A3A.1 ZC123.3 ZC123.2

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 119 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZC123.3 and has the DNA sequence

TTGAGAACTCTGCGTCTCAACTCCCGCATTTTTTGTAGATCTACGTAGATC
AAACCGAAATGGGACACT

A C1/C2 short loop on chromosome 1 whose identifier is 122 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZC123.3 and has the DNA sequence

GCACGGGGTTCTGGCCTTCCTCATTGAATTTTTCGCGCTCCATTGACAATC
GCCTGCCGGACAACGCGTGGGAAAGTCGTGTACTCCAC

A C1/C2 short loop on chromosome 1 whose identifier is 125 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZC123.3 and has the DNA sequence

ACGCGCCGTAAATCTACCCCAGATATGGCCGAGCCAAAATGGCCTAGTTC
GGCAAACTCTTTCATTTCAATTTATGAGGGAAGCCAGAA

A C1/C2 short loop on chromosome 1 whose identifier is 130 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZC123.2 and has the DNA sequence

CTCCCGCATTTTTTGTAGATCTACGTAGATCAAACCGAAATGAGGCACTTT
CTGAATCCACGAGCTAGGCTTAAGCTTAGGCTTAAGCTTAGGCCTTTTCTC
AGGCTTAGGCTTAGGCTTA

A C1/C2 short loop on chromosome 1 whose identifier is 132 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZC123.2 and has the DNA sequence

GCTTATGCTTGGGCTTAGGCTTAGGCGTAGGCTTAGGCTTAGGCTTAGGCT
TATGCTTAGACTTAGTCTCACTATCAGTCTTAGGCTTAGGCTTAGACTTAG
GCTTAAGCTTAGGCTTAAGCTTAGACTTAGGCTTAGGCTTAGGCTTAGGCT
TAGGCTTAGGTTTGGGCTTAGGCTTAGGCTTAACCTC

A C1/C2 short loop on chromosome 1 whose identifier is 134 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZC123.2 and has the DNA sequence

TCTGCGTCTTTTCTCCCGCATTTTTTGTAGATCTACGTAGATCAAACCGAA
ATGAGGCACTTTCTGAATCCACGAGCTAGGCTTAAGCTTAGGCTTAAGCTT
AGGCCTTTTCTCAGGCTTAGGCTTAGGCTTA

A C1/C2 short loop on chromosome 1 whose identifier is 136 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZC123.2 and has the DNA sequence

GCTTATGCTTGGGCTTAGGCTTAGGCGTAGGCTTAGGCTTAGGCTTAGGCT
TATGCTTAGACTTAGTCTCACTATCAGTCTTAGGCTTAGGCTTAGACTTAG
GCTTAAGCTTAGGCTTAAGCTTAGACTTAGGCTTAGGCTTAGGCTTAGGCT
TAGGCTTAGGTTTGGGCTTAGGCTTAGGCTTAACCTC

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 5 whose identifier is 21719 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene C39F7.5 and has the DNA sequence

ACGTTCTTAACCATGCAAAATCAGTTGAGAACTCTGCGTCTCTTCTCCCGC
ATTTTTTGTAGATC

The match between the T1 sequence and the C1/C2 sequence is

ACGTTCTTAACCATGCAAAATCAGTTGAGAACTCTGCGTCTCTTCTCCCGC

The match between the T2 sequence and the C1/C2 sequence is

ACTCTGCGTCTCTTCTCCCGCATTTTTTGTAGATC

A C1/C2 short loop on chromosome 5 whose identifier is 21949 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene F16B4.4 and has the DNA sequence

ACCATGCAAAATCAGTTGAGAACTCTGCGTCTCTTCTCCCGCATTTTTTGT
AGATCTACGTAGATCAAGCCGAAATGAGACACTCTGACACCACG

The match between the T1 sequence and the C1/C2 sequence is

ACCATGCAAAATCAGTTGAGAACTCTGCGTCTCTTCTCCCGC

The match between the T2 sequence and the C1/C2 sequence is

ACTCTGCGTCTCTTCTCCCGCATTTTTTGTAGATC

A C1/C2 short loop on chromosome 5 whose identifier is 21655 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene C39F7.3 and has the DNA sequence

AACCATGCAAAATCAGTTGAGAACTCTGCGTCTCTTCTCCCGCATTTTTTG
TAGATCTACG

The match between the T1 sequence and the C1/C2 sequence is

AACCATGCAAAATCAGTTGAGAACTCTGCGTCTCTTCTCCCGC

The match between the T2 sequence and the C1/C2 sequence is

ACTCTGCGTCTCTTCTCCCGCATTTTTTGTAGATC

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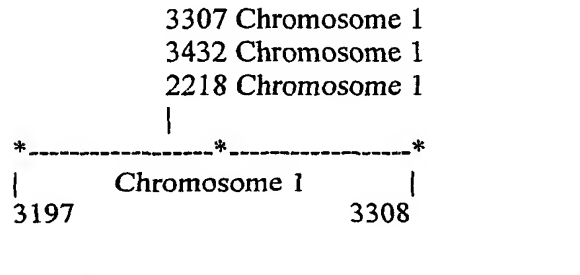
2. Many Connectrons control the expression of one set of genes in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

Many different C1/C2 short loops can control the existence of one T1-T2 long loop. The C1/C2 short loops can be on the same chromosome or on different chromosomes from the T1-T2 long loop. This relationship is described as "many-to-one". This relationship exists in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes

Example of a many-to-one connectron in prokaryotes – E. coli

In this example the existence of the T1-T2 (3197-3308) long loop is controlled by three C1/C2 short loops (3307, 3432 and 2218).



A double stranded DNA loop of length 93.542 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3197. This T1 control element has the DNA sequence

AAAAAATGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGG
AATAACTCCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACG
CCGCCGGGTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAA
ATAAATGCTTGACTCTGTAGCGGGAA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3308. This T2 control element has the DNA sequence

TAAATTTCCTCTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTG
ACACGGAACAACGGCAAACACGCCGCCGGGTCAGCGGGGTTCTCCTGAG
AACTCCGGCAGAGAAAGCAAAAATAAATGCTTGACTCTGTAGCGGGAAG
GCGTATTATGCACACCCCGCGCCGCT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

rrsC	gltU	rrlC	rrfC	aspT	trpT	yifA	yifE	yifB
ilvL	ilvG_1	ilvM	ilvE	ilvD	ilvA	ilvY	ilvC	ppiC
b3776	rep	gppA	rhlB	trxA	rhoL	rho	rfe	wzzE
wecB	rffH	wecD	wecE	wzxE	yifM_2	wecG	yifK	
argX	hisR	leuT	proM	aslB	aslA	hemY	hemX	
hemD	cyaA	cyaY	b3808	dapF	uvrD	b3814	corA	
yigF	yigG	rarD	yigI	pldA	recQ	yigJ	yigK	pldB
yigL	yigM	metR	metE	ysgA	udp	yigN	ubiE	yigP
b3836	yigU	yigW_1	rfaH	yigC	ubiB	fadA	fadB	
pepQ	trkH	hemG						

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 3307 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene hemG and has the DNA sequence

AAAAAATGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGG
AATAACTCCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACG
CCGCCGGGTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAA
ATAAATGCTTGACTCTGTAGCGGGAAGGCGTATTATG...GGAGTCTGCAAC
TCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACG

GTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGT
GGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACT
TTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTAGGGGAAC
CTGCGGTTGGATCACCTCCTTACCTTAAAGAAGCGTTCTTTG

The match between the T1 sequence and the C1/C2 sequence is

AAAAAATGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGG
AATAACTCCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACG
CCGCCGGGTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAA
ATAAATGCTTGACTCTGTAGCGGGAA

The match between the T2 sequence and the C1/C2 sequence is

TAAATTTCCTCTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTG
ACACGGAACAACGGCAAACACGCCGCCGGGTCAGCGGGGTTCTCCTGAG
AACTCCGGCAGAGAAAGCAAAAATAAATGCTTGACTCTGTAGCGGGAAG
GCGTATTATGCACACCCCGCGCCGCT

A C1/C2 short loop on chromosome 1 whose identifier is 3432 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene btuB and has the DNA sequence

TGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGGAATAACT
CCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACGCCGCCGG
GTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAAATAAATG
CTTGACTCTGTAGCGGGAAGGCGTATTATGCACACC...ACACCATGGGAGT
GGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACT
TTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTAGGGGAAC
CTGCGGTTGGATCACCTCCTTACCTTAAAGAAGCGT

The match between the T1 sequence and the C1/C2 sequence is

TGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGGAATAACT
CCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACGCCGCCGG
GTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAAATAAATG
CTTGACTCTGTAGCGGGAA

The match between the T2 sequence and the C1/C2 sequence is

TAAATTTCCTCTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTG
ACACGGAACAACGGCAAACACGCCGCCGGGTCAGCGGGGTTCTCCTGAG
AACTCCGGCAGAGAAAGCAAAAATAAATGCTTGACTCTGTAGCGGGAAG
GCGTATTATGCACACCCCGCGCCGCT

A C1/C2 short loop on chromosome 1 whose identifier is 2218 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene clpB and has the DNA sequence

CTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTGACACGGAAC
AACGGCAAACACGCCGCCGGGC

The match between the T1 sequence and the C1/C2 sequence is

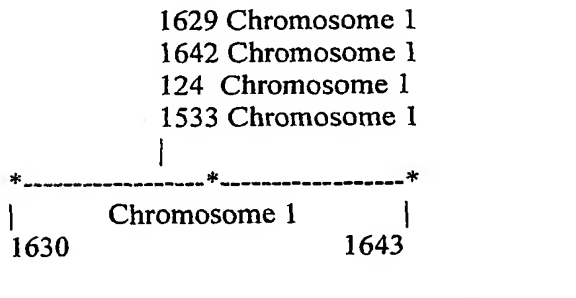
CTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTGACACGGAAC
AACGGCAAACACGCCGCCGGGC

The match between the T2 sequence and the C1/C2 sequence is

CTTGTCAGGCCGGAATAACTCCCTATAATGCGCCACCACTGACACGGAAC
AACGGCAAACACGCCGCCGGGC

Example of a many-to-one connectron in archea – M. jannaschii

In this example the existence of the T1-T2 (1630-1643) long loop is controlled by four C1/C2 short loops (1629, 1642, 124 and 1533).



A double stranded DNA loop of length 4.998 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 1630. This T1 control element has the DNA sequence

TTATTAATTAGTTCAAAGGATTTTTATTTAATTTCTAAGGGTTTGCTGGTTT
GATTATTTAGAATATTTGAGTTTATTGAATTATTCAGATTTTTAAAAATTA
AGATTAATTAGGAAAGGAAATAAGATTTCTCTAACAGACAAGTTAAATTT
TTGGATTTAAAAAGATAAAAAT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1643. This T2 control element has the DNA sequence

TTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTATTG
AATTATTCAGATTTTTAAAAATTAGGATTAATTAGGCAAGTAAATAAAAT
TTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATAAAAATACTCT
GTTTTATTATGGAAAGAAAGAT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

MJ1597 MJ1598 MJ1599 MJ1600 MJ1601 MJ1602

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 1629 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1597 and has the DNA sequence

ATATGTTTGAAATTTGAAAATAAGAGTATTTAGAAGTTATTAATTAGTTCA
AAGGATTTTTATTTAATTTCTAAGGGTTTGCTGGTTTGATTATTTAGAATAT
TTGAGTTTATTGAATTATTCAGATTTTTAAAAATTA

The match between the T1 sequence and the C1/C2 sequence is

TTATTAATTAGTTCAAAGGATTTTTATTTAATTTCTAAGGGTTTGCTGGTTT
GATTATTTAGAATATTTGAGTTTATTGAATTATTCAGATTTTTAAAAATTA

The match between the T2 sequence and the C1/C2 sequence is

GCTGGTTTGATTATTTAGAATATTTGAGTTTATTGAATTATTCAGATTTTTA
AAAATTA

A C1/C2 short loop on chromosome 1 whose identifier is 1642 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1602 and has the DNA sequence

ATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATTATTCAGATTTTTTAAAAATTAGGATTAATTAGGCAAGTAAATAAA
ATTTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATAAAAATACT
CTGTTTTATTATGGAAAGAAAGAT

The match between the T1 sequence and the C1/C2 sequence is

GCTGGTTTGATTATTTAGAATATTTGAGTTTATTGAATTATTCAGATTTTTA
AAAATTA

The match between the T2 sequence and the C1/C2 sequence is

TTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTATTG
AATTATTCAGATTTTTAAAAATTAGGATTAATTAGGCAAGTAAATAAAAT
TTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATAAAAATACTCT
GTTTTATTATGGAAAGAAAGAT

A C1/C2 short loop on chromosome 1 whose identifier is 124 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ0112 and has the DNA sequence

ATTTAATTTCTAAGGGTTTGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATTATTCAGATTTTTAAAAT

The match between the T1 sequence and the C1/C2 sequence is

ATTTAATTTCTAAGGGTTTGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATTATTCAGATTTTTAAAAT

The match between the T2 sequence and the C1/C2 sequence is

GCTGGTTTGATTATTTAGAATATTTGAGTTTATTGAATTATTCAGATTTTTA
AAAAT

A C1/C2 short loop on chromosome 1 whose identifier is 1533 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1486 and has the DNA sequence

TTTTTATTTAATTTCTAAGGGTTTGCTGGTTTGATTATTTAGAATATTTGAG TTTATT

The match between the T1 sequence and the C1/C2 sequence is

TTTTTATTTAATTTCTAAGGGTTTGCTGGTTTGATTATTTAGAATATTTGAG TTTATT

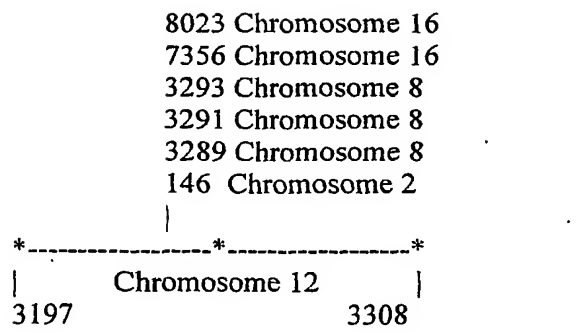
The match between the T2 sequence and the C1/C2 sequence is

GCTGGTTTGATTATTTAGAATATTTGAGTTTATT

Example of a many-to-one connectron in single-cell eukaryotes – S. cervesiae

In this example the existence of the T1-T2 (5515-5533) long loop on chromosome 12 is controlled by seventeen C1/C2 short loops (5516, 5532, 1939, 2323, 1942, 3286, 3649, 4764, 4751, 5536, 6102, 8023, 7356, 3293, 3291, 3289 and 146).

5516 Chromosome 12
5532 Chromosome 12
1939 Chromosome 4
2323 Chromosome 5
1942 Chromosome 5
3286 Chromosome 7
3649 Chromosome 8
4764 Chromosome 12
4751 Chromosome 12
5536 Chromosome 13
6102 Chromosome 14



A double stranded DNA loop of length 6.466 kilo-bases on chromosome 12 is bounded on the left by a T1 sequence whose identifier is 5515. This T1 control element has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 5533. This T2 control element has the DNA sequence

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

YLR467W

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 12 whose identifier is 5516 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YLR464W and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

A C1/C2 short loop on chromosome 12 whose identifier is 5532 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YLR467W and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 4 whose identifier is 1939 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed

as a RNA single strand that is 3'UTR to the gene YDR545W and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGG

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGG

A C1/C2 short loop on chromosome 5 whose identifier is 2323 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YER189W and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG

GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTA
AGAGACAACAGGGCT

A C1/C2 short loop on chromosome 5 whose identifier is 1942 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YEL077C and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTA
AGAGACAACAGGGCT

A C1/C2 short loop on chromosome 7 whose identifier is 3286 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YGR296W and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG

GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

A C1/C2 short loop on chromosome 8 whose identifier is 3649 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YHR219W and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

A C1/C2 short loop on chromosome 12 whose identifier is 4764 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YLL066C and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

A C1/C2 short loop on chromosome 12 whose identifier is 4751 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YLL067C and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

A C1/C2 short loop on chromosome 13 whose identifier is 5536 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YML133C and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

A C1/C2 short loop on chromosome 14 whose identifier is 6102 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YNL339C and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG

GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

A C1/C2 short loop on chromosome 16 whose identifier is 8023 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YPR204W and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

A C1/C2 short loop on chromosome 16 whose identifier is 7356 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YPL283C and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

A C1/C2 short loop on chromosome 8 whose identifier is 3293 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YHL050C and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTT

The match between the T1 sequence and the C1/C2 sequence is

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTT

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTT

A C1/C2 short loop on chromosome 8 whose identifier is 3291 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YHL050C and has the DNA sequence

ATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGC
GAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAA

The match between the T1 sequence and the C1/C2 sequence is

ATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGC
GAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAA

The match between the T2 sequence and the C1/C2 sequence is

ATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGC
GAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAA

A C1/C2 short loop on chromosome 2 whose identifier is 145 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YBL113C and has the DNA sequence

CTATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAAC
ATCCGGGTAAGAGACAACAGGCT

The match between the T1 sequence and the C1/C2 sequence is

CTATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

CTATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAAC
ATCCGGGTAAGAGACAACAGGCT

A C1/C2 short loop on chromosome 8 whose identifier is 3289 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed

as a RNA single strand that is 3'UTR to the gene YHL050C and has the DNA sequence

CTATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAAC
ATCCGGGTAAGAGACAACAGGCT

The match between the T1 sequence and the C1/C2 sequence is

CTATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

CTATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAAC
ATCCGGGTAAGAGACAACAGGCT

A C1/C2 short loop on chromosome 2 whose identifier is 146 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YBL113C and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAA

The match between the T1 sequence and the C1/C2 sequence is

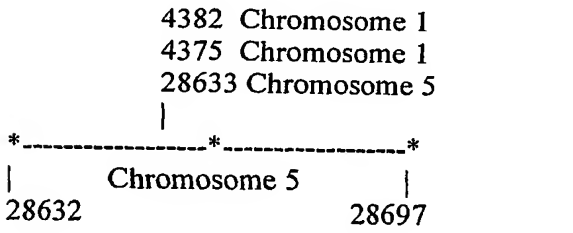
AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAA

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAA

Example of a many-to-one connectron in multi-cell eukaryotes – C. elegans

In this example the existence of the T1-T2 (3197-3308) long loop on chromosome 5 is controlled by three C1/C2 short loops (4382, 4375 and 28633).



A double stranded DNA loop of length 58.451 kilo-bases on chromosome 5 is bounded on the left by a T1 sequence whose identifier is 28632. This T1 control element has the DNA sequence

GCAAAAATTGACTGAAAATTTGAATTTCCCGCAAAAAATTGACTGAAAAT
TTGAATTTCCCGCCAAAAATTGACTGAAAATTTGAA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 28697. This T2 control element has the DNA sequence

CAAAAAATTGACTGAAAATTTGAATTTCCCTCCAAAAATTGACTGAAAAT
TTGAATTTCCCGCCAAAAATTGACTGAAAATTTGAATATCCCGCCAAAAA
TTGACTGAAAATTTGAATTTCCCGCCGAAAATTAAATGAAAAATGGAATT
TCTCGCCGAA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

M162.8 M162.4 M162.3 M162.6 M162.2 M162.1 M162.7

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 4382 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene Y43F8B.10 and has the DNA sequence

ATTATAGAAAATTTAAATTTCCCTCCAAAAAATTGACTGAAAATTTGAATT
TCCCTCCAAAAATTGACTGAAAATTTGAATTTCCCGCCAAAAATTGACTG
AAAATTTGAATATCCCGCCAAAAATTGACTGAAAATTTGAATTTCCCGCC
GAAAATTAAATGAAAAATGGAATTTCTCGCCGAAAAATTCAGTAAAAATT
TGAATTTCCTGCCAAAAATTGACTGAAAATTTGAATTTCTTGCCAAAAAA
GTGACTGGGAATTTGAATTTCCCTCCAAAAATTGACTGAAATTTTGAATTT
CCCGCTAAAAGTTGACT

The match between the T1 sequence and the C1/C2 sequence is

CAAAAATTGACTGAAAATTTGAATTTCCCGC

The match between the T2 sequence and the C1/C2 sequence is

CAAAAAATTGACTGAAAATTTGAATTTCCCTCCAAAAATTGACTGAAAAT
TTGAATTTCCCGCCAAAAATTGACTGAAAATTTGAATATCCCGCCAAAAA
TTGACTGAAAATTTGAATTTCCCGCCGAAAATTAAATGAAAAATGGAATT
TCTCGCCGAA

A C1/C2 short loop on chromosome 1 whose identifier is 4375 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed

as a RNA single strand that is 3'UTR to the gene Y43F8B.10 and has the DNA sequence

ATTATAGAAAATTTAAATTTCCCTCCAAAAAATTGACTGAAAATTTGAATT
TCCCTCCAAAAATTGACTGAAAATTTGAATTTCCCGCCAAAAATTGACTG
AAAATTTGAATATCCCGCCAAAAATTGACTGAAAATTTGAATTTCCCGCC
GAAAATTAAATGAAAAATGGAATTTCTCGCCGAAAAATTCAGTAAAAATT
TGAATTTCCTGCCAAAAATTGACTGAAAATTTGAATTTCTTGCCAAAAAA
GTGACTGGGAATTTGAATTTCCCTCCAAAAATTGACTGAAATTTTGAATTT
CCCGCTAAAAGTTGACT

The match between the T1 sequence and the C1/C2 sequence is

CAAAAATTGACTGAAAATTTGAATTTCCCGC

The match between the T2 sequence and the C1/C2 sequence is

CAAAAAATTGACTGAAAATTTGAATTTCCCTCCAAAAATTGACTGAAAAT
TTGAATTTCCCGCCAAAAATTGACTGAAAATTTGAATATCCCGCCAAAAA
TTGACTGAAAATTTGAATTTCCCGCCGAAAATTAAATGAAAAATGGAATT
TCTCGCCGAA

A C1/C2 short loop on chromosome 5 whose identifier is 28633 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene M162.5 and has the DNA sequence

CAAAAATTGACTGAAAATTTGAATTTCCCGCAAAAAATTGACTGAAAATT
TGAATTTCCCGCCAAAAATTGACTGAAAATTTGAA

The match between the T1 sequence and the C1/C2 sequence is

CAAAAATTGACTGAAAATTTGAATTTCCCGCAAAAAATTGACTGAAAATT
TGAATTTCCCGCCAAAAATTGACTGAAAATTTGAA

The match between the T2 sequence and the C1/C2 sequence is

CAAAAAATTGACTGAAAATTTGAATTTCCC

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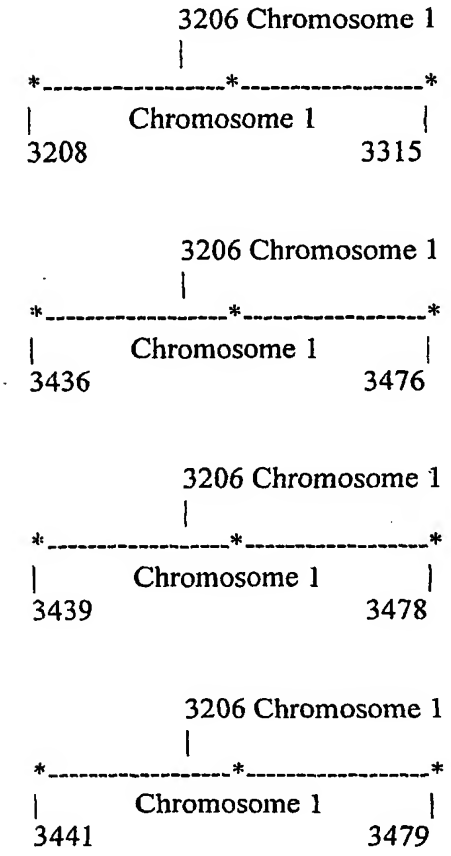
3. One connectron controls the expression of many sets of genes in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

One C1/C2 short loop can control the existence of a many T1-T2 long loops. The C1/C2 short loop can be on the same chromosome or on different chromosomes from the T1-T2 long loops. This relationship is described as "one-to-many". This relationship exists in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

Example of a one-to-many connectron in prokaryotes – E. coli

In this example the existence of T1-T2 (3208-3315, 3436-3476, 3439-3478 and 3441-3479) long loops are controlled by one C1/C2 short loop (3206).



A double stranded DNA loop of length 93.377 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3208. This T1 control element has the DNA sequence

ACTCATCTTCGGGTGATGTTTGAGATATTTGCTCTTTAAAAATCTGGATCA
AGCTGAAAATTGAAACACTGAACAACGAAAGTTGTTCGTGAGTCTCTCAA
ATTTTCGCAACACGATGATGAATCGAAAGAAACATCTTCGGGTTGTGAGG
TTAAGCGACTAAGCGTACACGGTGGATGCCCTGGC...AGTGTGTTTCGACA
CACTATCATTAACTGAATCCATAGGTTAATGAGGCGAACCGGGGGAACTG
AAACATCTAAGTACCCCGAGGAAAAGAAATCAACCGAGATTCCCCCAGTA
GCGGCGAGCGAACGGGGAGCAGCCCAGAGCCTGAATCAGT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3315. This T2 control element has the DNA sequence

TTTGCTCTTTAAAAATCTGGATCAAGCTGAAAATTGAAACACTGAACAAC
GAAAGTTGTTCGTGAGTCTCTCAAATTTTCGCAACTCTGAAGTGAAACATC
TTCGGGTTGTGAGGTTAAGCGACTAAGCGTACACGGTGGATGCCCTGGCA
GTCAGAGGCGATGAAGGACGTGCTAATCTGCGATA...GGTTAATGAGGCG
AACCGGGGGAACTGAAACATCTAAGTACCCCGAGGAAAAGAAATCAACC
GAGATTCCCCCAGTAGCGGCGAGCGAACGGGGAGCAGCCCAGAGCCTGA
ATCAGTGTGTGTGTTAGTGGAAGCGTCTGGAAA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

rrlC	rrfC	aspT	trpT	yifA	yifE	yifB	ilvL	ilvG_1
ilvM	ilvE	ilvD	ilvA	ilvY	ilvC	ppiC	b3776	rep
gppA	rhlB	trxA	rhoL	rho	rfe	wzzE	wecB	rffH

wecD wecE wzxE yifM_2 wecG yifK argX hisR
leuT proM aslB aslA hemY hemX hemD cyaA
cyaY b3808 dapF uvrD b3814 corA yigF yigG rarD
yigI pldA recQ yigJ yigK pldB yigL yigM metR
metE ysgA udp yigN ubiE yigP b3836 yigU
yigW_1 rfaH yigC ubiB fadA fadB pepQ trkH
hemG rrsA ileT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 3206 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrsC and has the DNA sequence

GTCCCCTTCGTCTAGAGGCCCAGGACACCGCCCTTTCACGGCGGTAACAG
GGGTTCGAATCCCCTAGGGGACGCCACTTGCTGGTTTGTGAGTGAAAGTC
ACCTGCCTTAATATCTCAAAACTCATCTTCGGGTGATGTTTGAGATATTTG
CTCTTTAAAAATCTGGATCAAGCTGAAAATTGAAA...ACCGGCGATTTCCG
AATGGGGAAACCCAGTGTGTTTCGACACACTATCATTAACTGAATCCATA
GGTTAATGAGGCGAACCGGGGGAACTGAAACATCTAAGTACCCCGAGGA
AAAGAAATCAACCGAGATTCCCCCAGTAGCGGCGAGCGAACGGGGAGCA
GCCCAGAGCCTGAATCAGT

The match between the T1 sequence and the C1/C2 sequence is

ACTCATCTTCGGGTGATGTTTGAGATATTTGCTCTTTAAAAATCTGGATCA
AGCTGAAAATTGAAACACTGAACAACGAAAGTTGTTCGTGAGTCTCTCAA
ATTTTCGCAACACGATGATGAATCGAAAGAAACATCTTCGGGTTGTGAGG
TTAAGCGACTAAGCGTACACGGTGGATGCCCTGGC...AGTGTGTTTCGACA
CACTATCATTAACTGAATCCATAGGTTAATGAGGCGAACCGGGGGAACTG

AAACATCTAAGTACCCCGAGGAAAAGAAATCAACCGAGATTCCCCCAGTA
GCGGCGAGCGAACGGGGAGCAGCCCAGAGCCTGAATCAGT

The match between the T2 sequence and the C1/C2 sequence is

TTTGCTCTTTAAAAATCTGGATCAAGCTGAAAATTGAAACACTGAACAAC
GAAAGTTGTTCGTGAGTCTCTCAAATTTTCGCAAC

A double stranded DNA loop of length 41.279 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3436. This T1 control element has the DNA sequence

ACGCAACGCGTGATAAGCAATTTTCGTGTCCCCTTCGTCTAGAGGCCCAG
GACACCGCCCTTTCACGGCGGTAACAGGGGTTCGAATCCCCTAGGGGACG
CCACTTGCTGGTT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3476. This T2 control element has the DNA sequence

AGTGAAAAGCAAGGCGTCTTGCGAAGCAGACTGATACGTCCCCTTCGTCT
AGAGGCCCAGGACACCGCCCTTTCACGGCGGTAACAGGGGTTCGAATCCC
CTAGGGGACGCCACTTGCTGGTTTGTGAGTGAAAGTCACCTGCCTTAATA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

gltT	rrlB	rrfB	murB	coaA	b3975	tyrU	thrT	tufB
secE	nusG	rplK	rplA	rplJ	rplL	rpoB	rpoC	htrC
thiH	thiF	thiE	yjaE	yjaD	hemE	nfi	yjaG	hupA
yjaH	yjaI	hydH	purD	purH				

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 3206 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrsC and has the DNA sequence

GTCCCCTTCGTCTAGAGGCCCAGGACACCGCCCTTTCACGGCGGTAACAG
GGGTTCGAATCCCCTAGGGGACGCCACTTGCTGGTTTGTGAGTGAAAGTC
ACCTGCCTTAATATCTCAAAACTCATCTTCGGGTGATGTTTGAGATATTTG
CTCTTTAAAAATCTGGATCAAGCTGAAAATTGAAACACTGAACAACGAAA
GTTGTTCGTGAGTCTCTCAAATTTTCGCAACACGATGATGAATCGAAAGA
AACATCTTCGGGTTGTGAGGTTAAGCGACTAAGCGTACACGGTGGATGCC
CTGGCAGTCAGAGGCGATGAAGGACGTGCTAATCTGCGATAAGCGTCGGT
AAGGTGATATGAACCGTTATAACCGGCGATTTCCGAATGGGGAAACCCAG
TGTGTTTCGACACACTATCATTAACTGAATCCATAGGTTAATGAGGCGAA
CCGGGGGAACTGAAACATCTAAGTACCCCGAGGAAAAGAAATCAACCGA
GATTCCCCCAGTAGCGGCGAGCGAACGGGGAGCAGCCCAGAGCCTGAAT
CAGT

The match between the T1 sequence and the C1/C2 sequence is

GTCCCCTTCGTCTAGAGGCCCAGGACACCGCCCTTTCACGGCGGTAACAG
GGGTTCGAATCCCCTAGGGGACGCCACTTGCTGGTT

The match between the T2 sequence and the C1/C2 sequence is

GTCCCCTTCGTCTAGAGGCCCAGGACACCGCCCTTTCACGGCGGTAACAG
GGGTTCGAATCCCCTAGGGGACGCCACTTGCTGGTTTGTGAGTGAAAGTC
ACCTGCCTTAATA

A double stranded DNA loop of length 41.336 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3439. This T1 control element has the DNA sequence

CCTTAATATCTCAAAACTCATCTTCGGGTGATGTTTGAGATATTTGCTCTTT
AAAAATCTGGATCAAGCTGAAAATTGAAACACTGAACAACGA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3478. This T2 control element has the DNA sequence

GTGATGTTTGAGATATTTGCTCTTTAAAAATCTGGATCAAGCTGAAAATTG
AAACACTGAACAACGAAAGTTGTTCGTGAGTCTCTCAAATTTT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

rrlB	rrfB	murB	coaA	b3975	tyrU	thrT	tufB	secE
nusG	rplK	rplA	rplJ	rplL	rpoB	rpoC	htrC	thiH
thiF	thiE	yjaE	yjaD	hemE	nfi	yjaG	hupA	yjaH
yjaI	hydH	purD	purH	gltV				

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 3206 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the generrsC and has the DNA sequence

GTCCCCTTCGTCTAGAGGCCCAGGACACCGCCCTTTCACGGCGGTAACAG
GGGTTCGAATCCCCTAGGGGACGCCACTTGCTGGTTTGTGAGTGAAAGTC

ACCTGCCTTAATATCTCAAAACTCATCTTCGGGTGATGTTTGAGATATTTG
CTCTTTAAAAATCTGGATCAAGCTGAAAATTGAAA...ACCGGCGATTTCCG
AATGGGGAAACCCAGTGTGTTTCGACACACTATCATTAACTGAATCCATA
GGTTAATGAGGCGAACCGGGGGAACTGAAACATCTAAGTACCCCGAGGA
AAAGAAATCAACCGAGATTCCCCCAGTAGCGGCGAGCGAACGGGGAGCA
GCCCAGAGCCTGAATCAGT

The match between the T1 sequence and the C1/C2 sequence is

CCTTAATATCTCAAAACTCATCTTCGGGTGATGTTTGAGATATTTGCTCTTT
AAAAATCTGGATCAAGCTGAAAATTGAAACACTGAACAACGA

The match between the T2 sequence and the C1/C2 sequence is

GTGATGTTTGAGATATTTGCTCTTTAAAAATCTGGATCAAGCTGAAAATTG
AAACACTGAACAACGAAAGTTGTTCGTGAGTCTCTCAAATTTT

A double stranded DNA loop of length 38.285 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3441. This T1 control element has the DNA sequence

AATTTTCGCAACACGATGATGAATCGAAAGAAACATCTTCGGGTTGTGAG
GTTAAGCGACTAAGCGTACACGGTGGATGCCCTGGCAGTCAGAGGCGATG
AAGGACGTGCTAATCTGCGATAAGCGTCGGTAAGGTGATATGAACCGTTA
TAACCGGCGATTTCCGAATGGGGAAACCCAGTGTGT...GATGAGAGAAGA
TTTTCAGCCTGATACAGATTAAATCAGAACGCAGAAGCGGTCTGATAAAA
CAGAATTTGCCTGGCGGCAGTAGCGCGGTGGTCCCACCTGACCCCATGCC
GAACTCAGAAGTGAAACGCCGTAGCGCCGATGGTAGTGTGGGGTCTCCCC
ATGCGAG

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3479. This T2 control element has the DNA sequence

AAGAAACATCTTCGGGTTGTGAGGTTAAGCGACTAAGCGTACACGGTGGA
TGCCCTGGCAGTCAGAGGCGATGAAGGACGTGCTAATCTGCGATAAGCGT
CGGTAAGGTGATATGAACCGTTATAACCGGCGATTTCCGAATGGGGAAAC
CCAGTGTGTTTCGACACACTATCATTAACTGAATCC...CAGATTAAATCAG
AACGCAGAAGCGGTCTGATAAAACAGAATTTGCCTGGCGGCAGTAGCGC
GGTGGTCCCACCTGACCCCATGCCGAACTCAGAAGTGAAACGCCGTAGCG
CCGATGGTAGTGTGGGGTCTCCCCATGCGAGAGTAGGGAACTGCCAGGCA
TCAAATTA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

rrlB	rrfB	murB	coaA	b3975	tyrU	thrT	tufB	secE
nusG	rplK	rplA	rplJ	rplL	rpoB	rpoC	htrC	thiH
thiF	thiE	yjaE	yjaD	hemE	nfi	yjaG	hupA	yjaH
yjaI	hydH	purD	purH	gltV				

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 3206controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrsC and has the DNA sequence

GTCCCCTTCGTCTAGAGGCCCAGGACACCGCCCTTTCACGGCGGTAACAG
GGGTTCGAATCCCCTAGGGGACGCCACTTGCTGGTTTGTGAGTGAAAGTC
ACCTGCCTTAATATCTCAAAACTCATCTTCGGGTGATGTTTGAGATATTTG
CTCTTTAAAAATCTGGATCAAGCTGAAAATTGAAA...ACCGGCGATTTCCG
AATGGGGAAACCCAGTGTGTTTCGACACACTATCATTAACTGAATCCATA

GGTTAATGAGGCGAACCGGGGGAACTGAAACATCTAAGTACCCCGAGGA
AAAGAAATCAACCGAGATTCCCCCAGTAGCGGCGAGCGAACGGGGAGCA
GCCCAGAGCCTGAATCAGT

The match between the T1 sequence and the C1/C2 sequence is

AATTTTCGCAACACGATGATGAATCGAAAGAAACATCTTCGGGTTGTGAG
GTTAAGCGACTAAGCGTACACGGTGGATGCCCTGGCAGTCAGAGGCGATG
AAGGACGTGCTAATCTGCGATAAGCGTCGGTAAGGTGATATGAACCGTTA
TAACCGGCGATTTCCGAATGGGGAAACCCAGTGTGTTTCGACACACTATC
ATTAACTGAATCCATAGGTTAATGAGGCGAACCGGGGGAACTGAAACATC
TAAGTACCCCGAGGAAAAGAAATCAACCGAGATTCCCCCAGTAGCGGCG
AGCGAACGGGGAGCAGCCCAGAGCCTGAATCAGT

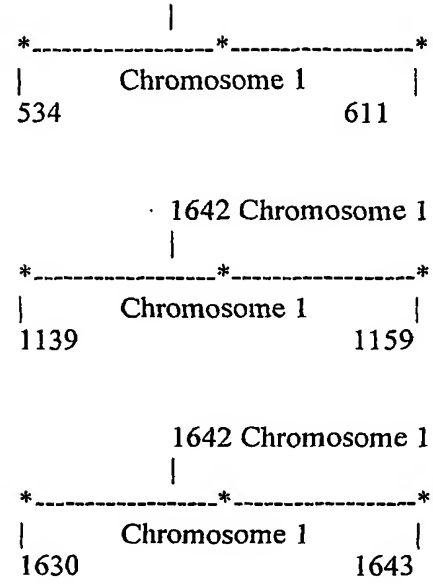
The match between the T2 sequence and the C1/C2 sequence is

AAGAAACATCTTCGGGTTGTGAGGTTAAGCGACTAAGCGTACACGGTGGA
TGCCCTGGCAGTCAGAGGCGATGAAGGACGTGCTAATCTGCGATAAGCGT
CGGTAAGGTGATATGAACCGTTATAACCGGCGATTTCCGAATGGGGAAAC
CCAGTGTGTTTCGACACACTATCATTAACTGAATCCATAGGTTAATGAGGC
GAACCGGGGGAACTGAAACATCTAAGTACCCCGAGGAAAAGAAATCAAC
CGAGATTCCCCCAGTAGCGGCGAGCGAACGGGGAGCAGCCCAGAGCCTG
AATCAGT

Example of a one-to-many connectron in archea – M. jannaschii

In this example the existence of T1-T2 (534-611, 1139-1159, and 1630-1643) long loops are controlled by one C1/C2 short loop (1642).

1642 Chromosome 1



A double stranded DNA loop of length 72.886 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 534. This T1 control element has the DNA sequence

TAAGTAAATAAAATTTCTCTAACAAATAAGTTAAATT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 611. This T2 control element has the DNA sequence

TAAATAAAATTTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATA AAAATGCT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

MJ0486	MJ0487	MJ0488	MJ0489	MJ0490	MJ0492	MJ0493
MJ0494	MJ0495	MJ0496	MJ0497	MJ0499	MJ0500	MJ0501

MJ0502 MJ0503 MJ0504 MJ0506 MJ0507 MJ0508 MJ0509
MJ0510 MJ0511 MJ0512 MJ0513 MJ0514 MJ0514 MJ0517
MJ0519 MJ0520 MJ0521 MJ0522 MJ0523 MJ0525 MJ0526
MJ0526 MJ0529 MJ0530 MJ0531 MJ0532 MJ0534 MJ0535
MJ0536 MJ0538 MJ0539 MJ0540 MJ0541 MJ0542 MJ0543
MJ0544 MJ0545 MJ0547 MJ0548 MJ0549 MJ0550 MJ0552
MJ0553 MJ0554 MJ0555 MJ0556 MJ0558 MJ0559 MJ0560
MJ0561 MJ0562 MJ0563 MJ0564

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 1642 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1602 and has the DNA sequence

ATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATTATTCAGATTTTTAAAAATTAGGATTAATTAGGCAAGTAAATAAA
ATTTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATAAAAATACT
CTGTTTTATTATGGAAAGAAAGAT

The match between the T1 sequence and the C1/C2 sequence is

AAGTAAATAAAATTTCTCTAACAAATAAGTTAAATT

The match between the T2 sequence and the C1/C2 sequence is

TAAATAAAATTTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATA
AAAAT

A double stranded DNA loop of length 14.509 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 1139. This T1 control element has the DNA sequence

ATTTATTAATTAGTTCAAAGGATTTTTATTTAATTTCTAAGGGTTAGCTGG
TTTGATTGTTTAAAATATTTGAGTTTA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1159. This T2 control element has the DNA sequence

ATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATTATTCAGATTTTTAAAAATTA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

MJ1096 MJ1097 tRNA-Arg-3 MJ1098 MJ1099 MJ1100 MJ1101
MJ1102 MJ1103 MJ1104 MJ1105 MJ1106 MJ1107 MJ1108

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 1642 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1602 and has the DNA sequence

ATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATTATTCAGATTTTTAAAAATTAGGATTAATTAGGCAAGTAAATAAA
ATTTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATAAAAATACT
CTGTTTTATTATGGAAAGAAAGAT

The match between the T1 sequence and the C1/C2 sequence is

ATTTAATTTCTAAGGGTTAGCTGGTTTGATT

The match between the T2 sequence and the C1/C2 sequence is

ATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATTATTCAGATTTTTAAAAATTA

A double stranded DNA loop of length 4.998 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 1630. This T1 control element has the DNA sequence

TTATTAATTAGTTCAAAGGATTTTTATTTAATTTCTAAGGGTTTGCTGGTTT
GATTATTTAGAATATTTGAGTTTATTGAATTATTCAGATTTTTAAAAATTA
AGATTAATTAGGAAAGGAAATAAGATTTCTCTAACAGACAAGTTAAATTT
TTGGATTTAAAAAGATAAAAAT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1643. This T2 control element has the DNA sequence

TTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTATTG
AATTATTCAGATTTTTAAAAATTAGGATTAATTAGGCAAGTAAATAAAAT
TTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATAAAAATACTCT
GTTTTATTATGGAAAGAAAGAT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

MJ1597 MJ1598 MJ1599 MJ1600 MJ1601 MJ1602

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 1642 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1602 and has the DNA sequence

ATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATTATTCAGATTTTTAAAAATTAGGATTAATTAGGCAAGTAAATAAA
ATTTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATAAAAATACT
CTGTTTTATTATGGAAAGAAAGAT

The match between the T1 sequence and the C1/C2 sequence is

GCTGGTTTGATTATTTAGAATATTTGAGTTTATTGAATTATTCAGATTTTTA
AAAATTA

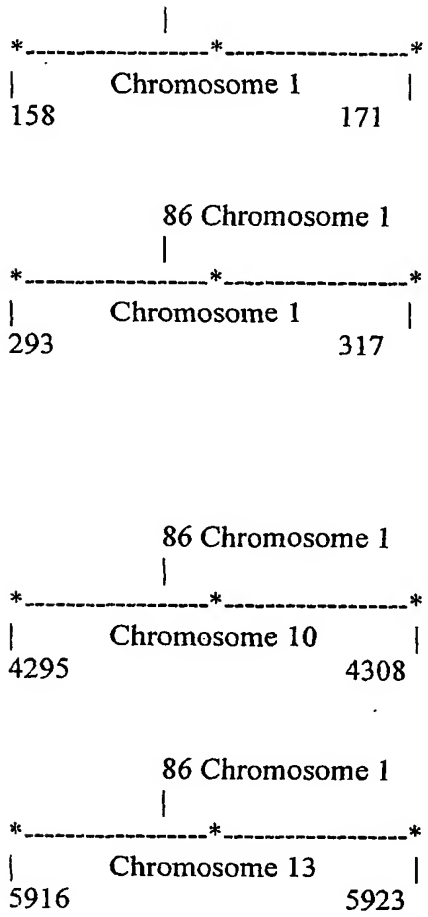
The match between the T2 sequence and the C1/C2 sequence is

TTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTATTG
AATTATTCAGATTTTTAAAAATTAGGATTAATTAGGCAAGTAAATAAAAT
TTCTCTAACAAATAAGTTAAATTTTTGGATTTAAAAAGATAAAAATACTCT
GTTTTATTATGGAAAGAAAGAT

Example of a one-to-many connectron in single-cell eukaryotes – S. cervesiae

In this example the existence of T1-T2 (158-171, 293-317, 4295-4308 and 5916-5923) long loops are controlled by one C1/C2 short loop (86).

86 Chromosome 1



A double stranded DNA loop of length 20.391 kilo-bases on chromosome 2 is bounded on the left by a T1 sequence whose identifier is 158. This T1 control element has the DNA sequence

CCAATTGTTGGAATAAAAATCAACTATCATCTACTAACTAGTATTTACGTT
ACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAGAA
ATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTAAT
AG

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 171. This T2 control element has the DNA sequence

ATAATTGTTGGAATAAAAATCAACTATCATCTACTAACTAGTATTTACGTT
ACTAGTATATTATCATATACGGTGTTAGAAGATGACACAAATGATGAGAA
ATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTAAT
AGGATCAATGAATATTAACATATAAAATGATGATAATAATA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

YBL107W-A TL(UAA)B1 YBL107C YBL106C YBL105C YBL104C YBL103C YBL102W YBL101C

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 86 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YAR009C and has the DNA sequence

ATCTATTACATTATGGGTGGTATGTTGGAATAGAAATCAACTATCATCTAC
TAACTAGTATTTACATTACTAGTATATTATCATATACGGTGTTAGAAGATG
ACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCTGAAACGCA
AGGATTGATAATGTAATAGGATCAATGAATATAAACATATAAAACGGAAT
GAGGAATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGAGG
ATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTAATATT
ATAGCCTTTATCAACAATGGAATCCCAACAATTATCTCAACATTCACCCAT
TTCTCAGAA

The match between the T1 sequence and the C1/C2 sequence is

AAATCAACTATCATCTACTAACTAGTATTTAC

The match between the T2 sequence and the C1/C2 sequence is

AAATCAACTATCATCTACTAACTAGTATTTAC

A double stranded DNA loop of length 38.470 kilo-bases on chromosome 2 is bounded on the left by a T1 sequence whose identifier is 293. This T1 control element has the DNA sequence

GAATTGTTGGAATAAAAATCCACTATCGTCTATCAACTAATAGTTATATTA
TCAATATATTATCATATACGGTGTTAAGATGATGACATAAGTTATGAGAA
GCTGTCATCGAAGTTAGAGGAAGCTGAAGTGCAAGGATTGATAATGTAAT
AGGATAATGAAACATATAAAACGGAATGAGGAATAATCGTAATATTAGT
ATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTTGAGGAGAAC
TTCTAGT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 317. This T2 control element has the DNA sequence

AATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTC
GAGGAGAACTTCTAGTATATTCTGTA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

YBL005W-B TS(AGA)B YBL004W YBL003C YBL002W YBL001C
YBR001C YBR002C YBR003W YBR004C YBR005W YBR006W
YBR007C YBR008C YBR009C YBR010W YBR011C YBR012C

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 86 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YAR009C and has the DNA sequence

ATCTATTACATTATGGGTGGTATGTTGGAATAGAAATCAACTATCATCTAC
TAACTAGTATTTACATTACTAGTATATTATCATATACGGTGTTAGAAGATG
ACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCTGAAACGCA
AGGATTGATAATGTAATAGGATCAATGAATATAAACATATAAAACGGAAT
GAGGAATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGAGG
ATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTAATATT
ATAGCCTTTATCAACAATGGAATCCCAACAATTATCTCAACATTCACCCAT
TTCTCAGAA

The match between the T1 sequence and the C1/C2 sequence is

AAACATATAAAACGGAATGAGGAATAATCGTAATATTAGTATGTAGAAAT
ATAGATTCCATTTTGAGGATTCCTATATCCT

The match between the T2 sequence and the C1/C2 sequence is

AATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTC
GAGGAGAACTTCTAGTATATTCTGTA

A double stranded DNA loop of length 11.020 kilo-bases on chromosome 10 is bounded on the left by a T1 sequence whose identifier is 4295. This T1 control element has the DNA sequence

AAACGCAAGGATTGATAATGTAATAGGATCAATGAATATAAACATATAAA
ACGGAATGAGGAATAATCGTAATATTAGTATGTAGAAATATAGATTCCAT
TTTGAGGATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTG

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 4308. This T2 control element has the DNA sequence

GGAAGCTGAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATAA
ACATATAAAACGGAATGAGGAATAATCGTAATATTAGTATGTAGAAATAT
AGATTCCATTTTGAGGATTCCTATATCCTCGAGGAGAACTTCTAGTATATT
CTGTATACCTAATATTATAGCCTTTATCAA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

YJR027W YJR029W

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 87 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YAR009C and has the DNA sequence

ATCTATTACATTATGGGTGGTATGTTGGAATAGAAATCAACTATCATCTAC
TAACTAGTATTTACATTACTAGTATATTATCATATACGGTGTTAGAAGATG
ACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCTGAAACGCA
AGGATTGATAATGTAATAGGATCAATGAATATAAACATATAAAACGGAAT
GAGGAATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGAGG
ATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTAATATT
ATAGCCTTTATCAACAATGGAATCCCAACAATTATCTCAACATTCACCCAT
TTCTCA

A double stranded DNA loop of length 5.462 kilo-bases on chromosome 13 is bounded on the left by a T1 sequence whose identifier is 5916. This T1 control element has the DNA sequence

AAGCTGAAGTGCAAGGATTGATAATGTAATAGGATAATGAAACATATAA
AACGGAATGAGGAATAATCGTAATATTAGTATGTAGAAATATAGATTCCA
TTTTGAGGATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 5923. This T2 control element has the DNA sequence

TAATAGGATAATGAAACATATAAAACGGAATGAGGAATAATCGTAATATT
AGTATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTCGAGGAG
AACTTCTAGTATATTCTGTATACCTAATATTATAGCCTTTATCAA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

YML045W

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

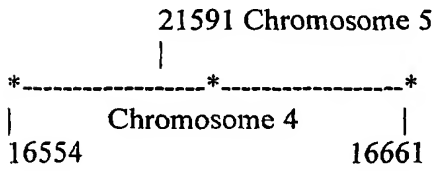
A C1/C2 short loop on chromosome 1 whose identifier is 87 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YAR009C and has the DNA sequence

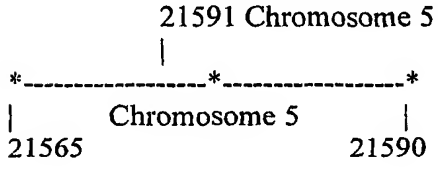
ATCTATTACATTATGGGTGGTATGTTGGAATAGAAATCAACTATCATCTAC
TAACTAGTATTTACATTACTAGTATATTATCATATACGGTGTTAGAAGATG

ACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCTGAAACGCA
AGGATTGATAATGTAATAGGATCAATGAATATAAACATATAAAACGGAAT
GAGGAATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGAGG
ATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTAATATT
ATAGCCTTTATCAACAATGGAATCCCAACAATTATCTCAACATTCACCCAT
TTCTCA

Example of a one-to-many connectron in multi-cell eukaryotes – C. elegans

In this example the existence of T1-T2 (16554-16661 and 21565-21590) long loops are controlled by one C1/C2 short loop (21591).





A double stranded DNA loop of length 50.159 kilo-bases on chromosome 4 is bounded on the left by a T1 sequence whose identifier is 16554. This T1 control element has the DNA sequence

TGCCTGAAAAAATTGGCTCCGAGTTAGGACACTTGGGGTGGTCAAAAAAT
TTTGTGACTATTGTCAAATGAAAGATCATAGTTGATAACATAAATTCCCAA
AGTTTCATAAAAATCGATACGCAGCGAACAAAGTTATCAATT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 16661. This T2 control element has the DNA sequence

CACTTGGGGTGGTCAAAAAATTTTGTGATTATTGTCAAATGAAAGATCAT
GGTTGATAACATAAATTCCCAAAGTTTCATAAAAATCGATACGCAGCGAA
CAAAGTTATGATTTTTGACCCGGAACTTATTTGGAGACCTA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

C23H5.7 C23H5.8a C23H5.3 C23H5.2 C23H5.9 C23H5.1

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 5 whose identifier is 21591 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene F25A2.1 and has the DNA sequence

TATTGTCAAATGAAAGATCATGGTTGATAACATAAATTCCCACAATTTCAT
AAAAATCGATACGCAGCGAACAAAGTTATGATTTTTGACCCGGAACTTAT
TTGGAGACCTAATATT

The match between the T1 sequence and the C1/C2 sequence is

TTTCATAAAAATCGATACGCAGCGAACAAAGTTAT

The match between the T2 sequence and the C1/C2 sequence is

TATTGTCAAATGAAAGATCATGGTTGATAACATAAATTCCCA

A double stranded DNA loop of length 18.142 kilo-bases on chromosome 5 is bounded on the left by a T1 sequence whose identifier is 21565. This T1 control element has the DNA sequence

CTCCGAGTTAGGACACTTGGGGTGGACAAAAAATTTTGTGACTATTGTCA
AATGAAAGATCATGGTTGATAA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 21590. This T2 control element has the DNA sequence

TATTGTCAAATGAAAGATCATGGTTGATAACATAAATTCCCACAATTTCAT
AAAAATCGATACGCAGCGAACAAAGTTATGATTTTTGACCCGGAACTTAT
TTGGAGACCTAATA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

T21H3.2 T21H3.1 F25A2.1

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 5 whose identifier is 21591 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene F25A2.1 and has the DNA sequence

TATTGTCAAATGAAAGATCATGGTTGATAACATAAATTCCCACAATTTCAT
AAAAATCGATACGCAGCGAACAAAGTTATGATTTTTGACCCGGAACTTAT
TTGGAGACCTAATATT

The match between the T1 sequence and the C1/C2 sequence is

TATTGTCAAATGAAAGATCATGGTTGATAA

The match between the T2 sequence and the C1/C2 sequence is

TATTGTCAAATGAAAGATCATGGTTGATAACATAAATTCCCACAATTTCAT
AAAAATCGATACGCAGCGAACAAAGTTATGATTTTTGACCCGGAACTTAT
TTGGAGACCTAATA

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4. Connectrons occur between prokaryotes and their plasmids.

Connectron relationships exist between prokaryotes and their plasmids. These connectrons implement a control mechanism between the two genomes that makes it possible for them to form a symbiotic relationship. In the case of D. radiodurans the relationship is not symmetric. The D. radiodurans genome sends C1/C2 short loops to the MP1 plasmid.

Example of a prokaryote/plasmid connectron – D. radiodurans

In this example the existence of T1-T2 (2654-2694 and 2692-2749) long loops in chromosome 3 that is the plasmid MP1 are controlled by one C1/C2 short loop (16) in chromosome 1.

```
              16  Chromosome 1
              2768 Chromosome 3 (plasmid MP1)
              2653 Chromosome 3 (plasmid MP1)
              |
*-----------------*-----------------*
|   Chromosome 3 (plasmid MP1)    |
2654                        2694
|          2693             |
```

```
              16  Chromosome 1
              2768 Chromosome 3 (plasmid MP1)
              2693 Chromosome 3 (plasmid MP1)
              |
*-----------------*-----------------*
|   Chromosome 3 (plasmid MP1)    |
2692                        2749
|        2693  2695          |
```

A double stranded DNA loop of length 46.903 kilo-bases on chromosome 3 (plasmid MP1) is bounded on the left by a T1 sequence whose identifier is 2654. This T1 control element has the DNA sequence

CAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCG
GTATGCAGCCTGCTCGGAGAGTACGATTCGTCGTTGGCTGCACCGAAGTG
ACGATGGGGCCATTCCGTGGGGCGCGTTACACCAGGCGACTGTCAGTACA
GCAATCGAGAGTGGGCTGATCAGCCCACTGTGCGTTCTGGCCATCGACGC
CTCTTTTCACCGCAAAGCCGGTCAGCACACCGCACACCTCGGCTCGTTCTG
GAATGGCTGTGCCGCGCGGACC

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 2694. This T2 control element has the DNA sequence

GCTGAACGCCCTGAATCTCTCCCGGTATGCAGCCTGCTCGGAGAGTACGA
TTCGTCGTTGGCTGCACCGAAGTGACGATGGGGCCATTCCGTGGGGCGCG
TTACACCAGGCGACTGTCAGTACAGCAATCGAGAGTGGGCTGATCAGCCC
ACTGTGCGTTCTGGCCATCGACGCCTCTTTTCACCGCAAAGCCGGTCAGCA
CACCGCACACCTCGGCTCGTTCTGGAATGGCTGTGCCGCGCGGACCGAAC
GCGGAATCGAGCAATCCTGTTGT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

DRB0020	DRB0021	DRB0022	DRB0023	DRB0024	DRB0025
DRB0027	DRB0030	DRB0032	DRB0033	DRB0034	DRB0035
DRB0037	DRB0038	DRB0039	DRB0041	DRB0042	DRB0043
DRB0044	DRB0045	DRB0047	DRB0051	DRB0052	DRB0054
DRB0055	DRB0057				

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 3 (plasmid MP1) whose identifier is 2693 controls the expression of the genes of one or more other T1/T2 long loops. This

C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DRB0057 and has the DNA sequence

CTGATGGCCATCCTACAGTACGTTCTCAGCGCGGTCCCGCTGCGCAAGAC
GCAGCGGAATTTCCTGACCGTGCTGCTCAGCGTTTTTCTCGCTGTTCCTGG
AC

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 16 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DR0009 and has the DNA sequence

GCTGTGAAATCACCGCTTCCAATGGGTCTGATGGCCATCCTACAGTACGTT
CTCAGCGCGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCT
GCTCAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTC
CCGGTATGCAGCCTGCTCGGAGAGTACGATTCGT

The match between the T1 sequence and the C1/C2 sequence is

CAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCG
GTATGCAGCCTGCTCGGAGAGTACGATTCGTCGTTGGCTGCACCGAAGTG
ACGATGGGGCCATTCCGTGGGGCGCGTTACACCAGGCGACTGTCAGTACA
GCAATCGAGAGTGGGCTGATCAGCCCACTGTGCGTTCTGGCCATCGACGC
CTCTTTTCACCGCAAAGCCGGTCAGCACACCGCACACCTCGGCTCGTTCTG
GAATGGCTGTGCCGCGCGGACC

The match between the T2 sequence and the C1/C2 sequence is

GCTGAACGCCCTGAATCTCTCCCGGTATGCAGCCTGCTCGGAGAGTACGA
TTCGTCGTTGGCTGCACCGAAGTGACGATGGGGCCATTCCGTGGGGCGCG
TTACACCAGGCGACTGTCAGTACAGCAATCGAGAGTGGGCTGATCAGCCC
ACTGTGCGTTCTGGCCATCGACGCCTCTTTTCACCGCAAAGCCGGTCAGCA
CACCGCACACCTCGGCTCGTTCTGGAATGGCTGTGCCGCGCGGACCGAAC
GCGGAATCGAGCAATCCTGTTGT

A C1/C2 short loop on chromosome 3 (plasmid MP1) whose identifier is 2768 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DRB0133 and has the DNA sequence

GCTGTGAAATCACCGCTTCCAATGGGTCTGATGGCCATCCTACAGTACGTT
CTCAGCGCGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCT
GCTCAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTC
CCGGTATGCAGCCTGCTCGGAGAGTACGATTCGT

The match between the T1 sequence and the C1/C2 sequence is

CAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCG
GTATGCAGCCTGCTCGGAGAGTACGATTCGTCGTTGGCTGCACCGAAGTG
ACGATGGGGCCATTCCGTGGGGCGCGTTACACCAGGCGACTGTCAGTACA
GCAATCGAGAGTGGGCTGATCAGCCCACTGTGCGTTCTGGCCATCGACGC
CTCTTTTCACCGCAAAGCCGGTCAGCACACCGCACACCTCGGCTCGTTCTG
GAATGGCTGTGCCGCGCGGACC

The match between the T2 sequence and the C1/C2 sequence is

GCTGAACGCCCTGAATCTCTCCCGGTATGCAGCCTGCTCGGAGAGTACGA
TTCGTCGTTGGCTGCACCGAAGTGACGATGGGGCCATTCCGTGGGGCGCG
TTACACCAGGCGACTGTCAGTACAGCAATCGAGAGTGGGCTGATCAGCCC

ACTGTGCGTTCTGGCCATCGACGCCTCTTTTCACCGCAAAGCCGGTCAGCA
CACCGCACACCTCGGCTCGTTCTGGAATGGCTGTGCCGCGCGGACCGAAC
GCGGAATCGAGCAATCCTGTTGT

A C1/C2 short loop on chromosome 3 (plasmid MP1) whose identifier is 2653 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DRB0017 and has the DNA sequence

CGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCTGCTCAGC
GTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCGGTAT
GCAGCCTGCTCGGAGAGTACGATTCGTCGTTGGCTGCACCGAAGTGACGA
TGGGGCCATTCCGTGGGGCGCGTTACACCAGGCGA

The match between the T1 sequence and the C1/C2 sequence is

CAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCG
GTATGCAGCCTGCTCGGAGAGTACGATTCGTCGTTGGCTGCACCGAAGTG
ACGATGGGGCCATTCCGTGGGGCGCGTTACACCAGGCGACTGTCAGTACA
GCAATCGAGAGTGGGCTGATCAGCCCACTGTGCGTTCTGGCCATCGACGC
CTCTTTTCACCGCAAAGCCGGTCAGCACACCGCACACCTCGGCTCGTTCTG
GAATGGCTGTGCCGCGCGGACC

The match between the T2 sequence and the C1/C2 sequence is

GCTGAACGCCCTGAATCTCTCCCGGTATGCAGCCTGCTCGGAGAGTACGA
TTCGTCGTTGGCTGCACCGAAGTGACGATGGGGCCATTCCGTGGGGCGCG
TTACACCAGGCGACTGTCAGTACAGCAATCGAGAGTGGGCTGATCAGCCC
ACTGTGCGTTCTGGCCATCGACGCCTCTTTTCACCGCAAAGCCGGTCAGCA
CACCGCACACCTCGGCTCGTTCTGGAATGGCTGTGCCGCGCGGACCGAAC
GCGGAATCGAGCAATCCTGTTGT

A double stranded DNA loop of length 68.612 kilo-bases on chromosome 3 (plasmid MP1) is bounded on the left by a T1 sequence whose identifier is 2692. This T1 control element has the DNA sequence

CTGATGGCCATCCTACAGTACGTTCTCAGCGCGGTCCCGCTGCGCAAGAC
GCAGCGGAATTTCCTGACCGTGCTGCTCAGCGTTTTTCTCGCTGTTCCTGG
AC

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 2749. This T2 control element has the DNA sequence

AGCGCGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCTGCT
CAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCG
GT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

DRB0059	DRB0060	DRB0061	DRB0062	DRB0064	DRB0065
DRB0066	DRB0067	DRB0068	DRB0069	DRB0070	DRB0072
DRB0073	DRB0074	DRB0076	DRB0077	DRB0079	DRB0080
DRB0081	DRB0083	DRB0085	DRB0086	DRB0087	DRB0088
DRB0089	DRB0090	DRB0092	DRB0093	DRB0094	DRB0096
DRB0097	DRB0098	DRB0102	DRB0103	DRB0104	DRB0105
DRB0106	DRB0107	DRB0111	DRB0112		

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 3 (plasmid MP1) whose identifier is 2693 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DRB0057 and has the DNA sequence

CTGATGGCCATCCTACAGTACGTTCTCAGCGCGGTCCCGCTGCGCAAGAC
GCAGCGGAATTTCCTGACCGTGCTGCTCAGCGTTTTTCTCGCTGTTCCTGG
AC

A C1/C2 short loop on chromosome 3 (plasmid MP1) whose identifier is 2695 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DRB0057 and has the DNA sequence

GCTGAACGCCCTGAATCTCTCCCGGTATGCAGCCTGCTCGGAGAGTACGA
TTCGTCGTTGGCTGCACCGAAGTGACGATGGGGCCATTCCGTGGGGCGCG
TTACACCAGGCGACTGTCAGTACAGCAATCGAGAGTGGGCTGATCAGCCC
ACTGTGCGTTCTGGCCATCGACGCCTCTTTTCACCGCAAAGCCGGTCAGCA
CACCGCACACCTCGGCTCGTTCTGGAATGGCTGTGCCGCGCGGACCGAAC
GCGGAATCGAGCAATCCTGTTGT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 16 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DR0009 and has the DNA sequence

GCTGTGAAATCACCGCTTCCAATGGGTCTGATGGCCATCCTACAGTACGTT
CTCAGCGCGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCT
GCTCAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTC
CCGGTATGCAGCCTGCTCGGAGAGTACGATTCGT

The match between the T1 sequence and the C1/C2 sequence is

CTGATGGCCATCCTACAGTACGTTCTCAGCGCGGTCCCGCTGCGCAAGAC
GCAGCGGAATTTCCTGACCGTGCTGCTCAGCGTTTTTCTCGCTGTTCCTGG
AC

The match between the T2 sequence and the C1/C2 sequence is

AGCGCGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCTGCT
CAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCG
GT

A C1/C2 short loop on chromosome 3 (plasmid MP1) whose identifier is 2768 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DRB0133 and has the DNA sequence

GCTGTGAAATCACCGCTTCCAATGGGTCTGATGGCCATCCTACAGTACGTT
CTCAGCGCGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCT
GCTCAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTC
CCGGTATGCAGCCTGCTCGGAGAGTACGATTCGT...CGGACCGAACGCGGA
ATCGAGCAATCCTGTTGTGCCCTCATTGATGTCCAGCACCGGCAGGCCTTG
ACGGTCGATGTCCGTCAGACCCTGACCGGGTCTGAGGCTCCAACTCGTCT
GGAACAG

The match between the T1 sequence and the C1/C2 sequence is

CTGATGGCCATCCTACAGTACGTTCTCAGCGCGGTCCCGCTGCGCAAGAC
GCAGCGGAATTTCCTGACCGTGCTGCTCAGCGTTTTTCTCGCTGTTCCTGG
AC

The match between the T2 sequence and the C1/C2 sequence is

AGCGCGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCTGCT
CAGCGTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCG
GT

A C1/C2 short loop on chromosome 3 (plasmid MP1) whose identifier is 2693 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DRB0057 and has the DNA sequence

CTGATGGCCATCCTACAGTACGTTCTCAGCGCGGTCCCGCTGCGCAAGAC
GCAGCGGAATTTCCTGACCGTGCTGCTCAGCGTTTTTCTCGCTGTTCCTGG
AC

The match between the T1 sequence and the C1/C2 sequence is

CTGATGGCCATCCTACAGTACGTTCTCAGCGCGGTCCCGCTGCGCAAGAC
GCAGCGGAATTTCCTGACCGTGCTGCTCAGCGTTTTTCTCGCTGTTCCTGG
AC

The match between the T2 sequence and the C1/C2 sequence is

AGCGCGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCTGCT
CAGCGTTTTTCTCGCTGTTCCTGGAC

A C1/C2 short loop on chromosome 3 (plasmid MP1) whose identifier is 2653 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene DRB0017 and has the DNA sequence

CGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCTGCTCAGC
GTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCGGTAT
GCAGCCTGCTCGGAGAGTACGATTCGTCGTTGGCTGCACCGAAGTGACGA
TGGGGCCATTCCGTGGGGCGCGTTACACCAGGCGA

The match between the T1 sequence and the C1/C2 sequence is

CGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCTGCTCAGC
GTTTTTCTCGCTGTTCCTGGAC

The match between the T2 sequence and the C1/C2 sequence is

CGGTCCCGCTGCGCAAGACGCAGCGGAATTTCCTGACCGTGCTGCTCAGC
GTTTTTCTCGCTGTTCCTGGACGGCTGAACGCCCTGAATCTCTCCCGGT

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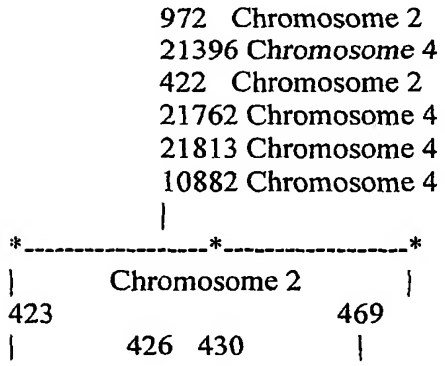
5. Connectrons occur in plants and higher animals

Connectron relationships exist in plant and higher animals.

Example of a plant connectron – A. thaliania

In this example the existence of the T1-T2 (423-469) long loop is controlled by six C1/C2 short loops (972, 21396, 422, 21762, 21813 and 10882). The T1-T2 long loop controls the expression of six genes on chromosome 2 in addition to two C1/C2 (426 and 430) short loops.



A double stranded DNA loop of length 42.285 kilo-bases on chromosome 2 is bounded on the left by a T1 sequence whose identifier is 423. This T1 control element has the DNA sequence

TATCTCTTTAAGGATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTA
ATTAAAAAACGAAATA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 469. This T2 control element has the DNA sequence

TACTAATTTAATTAATTAAATTTAATTAAAAAACGAAATACATTATTAATT
TTCAAAAATAATAACC

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

At2g02070 At2g02080 At2g02090 At2g02100 At2g02120 At2g02130

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 2 whose identifier is 426 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene At2g02060 and has the DNA sequence

TTCCAAAAATAATAACCAATCAAAATCAACATATAAGATTTGATATCTAA
ATTTT

A C1/C2 short loop on chromosome 2 whose identifier is 430 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene At2g02060 and has the DNA sequence

TTGCGGAAAAATAATATCATCATTATAAAAAAATAATTAGAGTTTTTTCGC
ATAT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 2 whose identifier is 972 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene At2g04240 and has the DNA sequence

GTATGCCATTAGAAATAAAATTTTAAAAGTAAATTAATTCATCTCTTTAAA
AATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTAATTAAAAAACG
AAATACATTATTAATTT

The match between the T1 sequence and the C1/C2 sequence is

ATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTAATTAAAAAACGA
AATA

The match between the T2 sequence and the C1/C2 sequence is

TACTAATTTAATTAATTAAATTTAATTAAAAAACGAAATACATTATTAATT
T

A C1/C2 short loop on chromosome 4 whose identifier is 21396 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene AT4g15300 and has the DNA sequence

TGCCATTAGAAATAAAATTTTAAAGAGTAAATTAATTTATCTCTTTAAGGA
TTAAAAAGTCAAATACTAATTTAATTAATTAAATTTAATTAAAAAACGAA
ATACATTATTAATTTCCAAAA

The match between the T1 sequence and the C1/C2 sequence is

TATCTCTTTAAGGATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTA
ATTAAAAAACGAAATA

The match between the T2 sequence and the C1/C2 sequence is

TACTAATTTAATTAATTAAATTTAATTAAAAAACGAAATACATTATTAATT
T

A C1/C2 short loop on chromosome 2 whose identifier is 422 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene At2g02060 and has the DNA sequence

TAACCTTAATTTTTGTAAGTAATTATATAGGTATGCCATTAGAAATAAAAT
TTTAAAGAGTAAATTAATTTATCTCTTTAAGGATTAAAAAGTCAAATACTA
ATTTAATTAATTAAATTTAATTAAAAAACGAAATA

The match between the T1 sequence and the C1/C2 sequence is

TATCTCTTTAAGGATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTA
ATTAAAAAACGAAATA

The match between the T2 sequence and the C1/C2 sequence is

TACTAATTTAATTAATTAAATTTAATTAAAAAACGAAATA

A C1/C2 short loop on chromosome 4 whose identifier is 21762 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene AT4g17510 and has the DNA sequence

TTTAAGGATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTAATTAAA
AAACGAAATACATT

The match between the T1 sequence and the C1/C2 sequence is

TTTAAGGATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTAATTAAA
AAACGAAATA

The match between the T2 sequence and the C1/C2 sequence is

TACTAATTTAATTAATTAAATTTAATTAAAAAACGAAATACATT

A C1/C2 short loop on chromosome 4 whose identifier is 21813 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene AT4g17680 and has the DNA sequence

TTTAAGGATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTAATTAAA
AAACGAAATACATT

The match between the T1 sequence and the C1/C2 sequence is

TTTAAGGATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTAATTAAA
AAACGAAATA

The match between the T2 sequence and the C1/C2 sequence is

TACTAATTTAATTAATTAAATTTAATTAAAAAACGAAATACATT

A C1/C2 short loop on chromosome 2 whose identifier is 10882 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene At2g26540 and has the DNA sequence

TATCTCTTTAAGGATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTA
ATTAA

The match between the T1 sequence and the C1/C2 sequence is

TATCTCTTTAAGGATTAAAAAGTCAAATACTAATTTAATTAATTAAATTTA
ATTAA

The match between the T2 sequence and the C1/C2 sequence is

TACTAATTTAATTAATTAAATTTAATTAA

Example of a animal connectron – D. megalomaster

A double stranded DNA loop of length 88.159 kilo-bases on chromosome 4 is bounded on the left by a T1 sequence whose identifier is 3340. This T1 control element has the DNA sequence

ACCTAAAAGAAGTACCGTTTTTTACTCCTAATTACCAATTCTAACCATCCA
TATCACTTTTTGACGGACTCCGTGAAAATAATTTTTGGCCAAATTTTCGCA
TTTTTTGTAAGGGGTAACATCATAAAAATT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3372. This T2 control element has the DNA sequence

AAAAAAGTACCGCGTTTTACTCCTAATTACCAATTCTAACCATCCATATCA
CTTTTTGACGGACTCCGTGAAAATAATTTTTGGCCAAATTTTCGCATTTTTT
GTAAGGGGTAACATCATCAAAATTTGCGAAAAA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

[Some of the following gene names have not been determined.]

- - - - -
- CG11207 - CG2186 CG2157
- Ork1 - - -
-

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 4 whose identifier is 3362 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene XXX and has the DNA sequence

AAAAAAGTACCGCGTTTTACTCCTAATTACCAATTCTAACCATCCATATCA
CTTTTTGACGGACTCCGTTAAAATAATTTTTGACCAAATTTTCGCATTTTTT
GTAATCAAAATTTGCAAAAAATTGAAAAAAC

A C1/C2 short loop on chromosome 4 whose identifier is 3364 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene XXX and has the DNA sequence

CAAAATTTGAATGCAAATCGATTGGGAATCAAAAAACAAACTCAACGAG
GTATGACATTCCATATTTGGGCCATTATTTCCAA

A C1/C2 short loop on chromosome 4 whose identifier is 3366 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene XXX and has the DNA sequence

TTTTTTCACAAAAATTAGGAAAATGATTTTGGGTAAAAAAATGAATATTT
AAGTTGGGTTTT

A C1/C2 short loop on chromosome 4 whose identifier is 3369 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene XXX and has the DNA sequence

AAATCGATTGGGAATCAAAAAACAAACCTCAACGAGGTATGACATTCCAT
ATCTGGGCCATTATTTCCAATCTTTTGATCAAAATAC

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 4 whose identifier is 3373 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene XXX and has the DNA sequence

AAAAAAGTACCGCGTTTTACTCCTAATTACCAATTCTAACCATCCATATCA
CTTTTTGACGGACTCCGTGAAAATAATTTTTGGCCAAATTTTCGCATTTTTT
GTAAGGGGTAACATCATCAAAATTTGCGAAAAA

The match between the T1 sequence and the C1/C2 sequence is

TTTTACTCCTAATTACCAATTCTAACCATCCATATCACTTTTTGACGGACTC
CGTGAAAATAATTTTTGGCCAAATTTTCGCATTTTTTGTAAGGGGTAACAT
CAT

The match between the T2 sequence and the C1/C2 sequence is

AAAAAAGTACCGCGTTTTACTCCTAATTACCAATTCTAACCATCCATATCA
CTTTTTGACGGACTCCGTGAAAATAATTTTTGGCCAAATTTTCGCATTTTTT
GTAAGGGGTAACATCATCAAAATTTGCGAAAAA

Example of an animal connectron – H. sapiens

All of the human genome that has been fully sequenced by both the NIH-lead global sequencing project and the Celera Genomics, Inc. project. The gene descriptors for this chromosome do not yet exist. Without the positions and directions of the genes, it is not possible to select from among the possible connectrons to determine the real connectrons.

Human chromosome 22 has been processed and there 31,000 possible connectrons.

The gene descriptors for all the chromosomes of the human genome should become available within the year.

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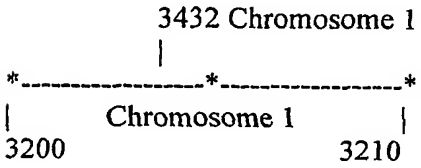
6. Permanent connectrons exist in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

C1/C2 short loops are normally expressed as the 3'UTR of some gene. A class of connectron relationships exist that permit one C1/C2 short loop to control the existence of one or more T1-T2 long loops without being subject to any expression controls other than those of the gene to which the C1/C2 is 3'UTR. These connectron relationships are described as "permanent". Permanent connectrons exist in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

Example of a prokaryote permanent connectron – E. coli

In this example the existence of the T1-T2 (3200-3210) long loop is controlled by a C1/C2 short loop (3432). The expression of this C1/C2 short loop is controlled only by the gene btuB.



A double stranded DNA loop of length 93.339 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3200. This T1 control element has the DNA sequence

AAGCGGCACTGCTCTTTAACAATTTATCAGACAATCTGTGTGGGCACTCG
AAGATACGGATTCTTAACGTCGCAAGACGAAAAATGAATACCAAGTCTCA
AGAGTGAACACGTAATTCATTACGAAGTTTAATTCTTTGAGCATCAAACTT
TTAAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCC
TAACACATGCAAGTCGAACGGTAACAGGAAACAGCTTGCTGTTTCGCTGA
CGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGG

GATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAA
GAGGGGGACCTTCGGGCCTCTTGCCATC

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3310. This T2 control element has the DNA sequence

CAGACAATCTGTGTGGGCACTCGAAGATACGGATTCTTAACGTCGCAAGA
CGAAAAATGAATACCAAGTCTCAAGAGTGAACACGTAATTCATTACGAAG
TTTAATTCTTTGAGCGTCAAACTTTTAAATTGAAGAGTTTGATCATGGCTC
AGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAACGGTAACA
GGAAGAAGCTTGCTTCTTTGCTGACGAGTGGCGGACGGGTGAGTAATGTC
TGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAAT
ACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCA
TCGGATGTGCCCAGATGGGATTAGCTAGT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

rrsC	gltU	rrlC	rrfC	aspT	trpT	yifA	yifE	yifB
ilvL	ilvG_1	ilvM	ilvE	ilvD	ilvA	ilvY	ilvC	ppiC
b3776	rep	gppA	rhlB	trxA	rhoL	rho	rfe	wzzE
wecB	rffH	wecD	wecE	wzxE	yifM_2	wecG	yifK	
argX	hisR	leuT	proM	aslB	aslA	hemY	hemX	
hemD	cyaA	cyaY	b3808	dapF	uvrD	b3814	corA	
yigF	yigG	rarD	yigI	pldA	recQ	yigJ	yigK	pldB
yigL	yigM	metR	metE	ysgA	udp	yigN	ubiE	yigP
b3836	yigU	yigW_1	rfaH	yigC	ubiB	fadA	fadB	
pepQ	trkH	hemG						

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 3432 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene btuB and has the DNA sequence

TGCGCGGTCAGAAAATTATTTTAAATTTCCTCTTGTCAGGCCGGAATAACT
CCCTATAATGCGCCACCACTGACACGGAACAACGGCAAACACGCCGCCGG
GTCAGCGGGGTTCTCCTGAGAACTCCGGCAGAGAAAGCAAAAATAAATG
CTTGACTCTGTAGCGGGAAGGCGTATTATGCACACC...TGCAACTCGACTC
CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATA
CGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGC
AAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACTTTGTGAT
TCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTAGGGGAACCTGCGGT
TGGATCACCTCCTTACCTTAAAGAAGCGT

The match between the T1 sequence and the C1/C2 sequence is

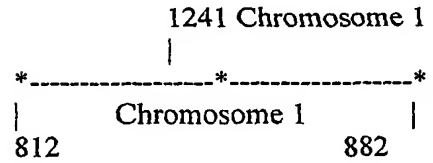
AAGCGGCACTGCTCTTTAACAATTTATCAGACAATCTGTGTGGGCACTCG
AAGATACGGATTCTTAACGTCGCAAGACGAAAAATGAATACCAAGTCTCA
AGAGTGAACACGTAATTCATTACGAAGTTTAATTCTTTGAGC

The match between the T2 sequence and the C1/C2 sequence is

CAGACAATCTGTGTGGGCACTCGAAGATACGGATTCTTAACGTCGCAAGA
CGAAAAATGAATACCAAGTCTCAAGAGTGAACACGTAATTCATTACGAAG
TTTAATTCTTTGAGCGTCAAACTTTTAAATTGAAGAGTTTGATCATGGCTC
AGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAACGGTAACA
GGAAGAAGCTTGCTTCTTTGCTGACGAGTGGCGGACGGGTGAGTAATGTC
TGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAAT
ACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCA
TCGGATGTGCCCAGATGGGATTAGCTAGT

Example of an archea permanent connectron – H. pylori

In this example the existence of the T1-T2 (812-882) long loop is controlled by a C1/C2 short loop (1241). The expression of this C1/C2 short loop is controlled only by the gene HP1535.



A double stranded DNA loop of length 96.385 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 812. This T1 control element has the DNA sequence

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 882. This T2 control element has the DNA sequence

TAGCGGAACTAAAGCATTCATCCCAAACACTAAAGATATTTGG

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

HP0999	HP1000	HP1001	HP1002	HP1003	HP1005	HP1006
HP1008	HP1009	HPtRNA-Pro	HP1010	HP1011	HP1013	HP1015
HP1017	HP1018	HP1020	HP1021	HP1022	HP1023	HP1024
HP1025	HP1027	HP1028	HP1030	HP1031	HP1033	HP1034
HP1038	HP1039	HP1040	HP1041	HP1042	HP1043	HP1044

HP1045	HP1046	HP1051	HP1052	HP1055	HP1056	HP1058
HP1060	HP1065	HPtRNA-Ser	HP1066	HP1067	HP1069	HP1070
HP1074	HP1075	HP1076	HP1077	HP1078	HP1079	HP1080
HP1081	HP1083	HP1084	HP1085	HP1088	HP1091	HP1092
HP1093	HP1094	HP1095	HP1096			

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 1241 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene HP1535 and has the DNA sequence

TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCATTCATCCC
AAACA

The match between the T1 sequence and the C1/C2 sequence is

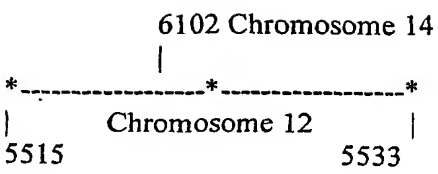
TTTTACTCATAGGGTTTTTATAGTTCCTAGCGGAACTAAAGCA

The match between the T2 sequence and the C1/C2 sequence is

TAGCGGAACTAAAGCATTCATCCCAAACA

Example of a single-celled permanent connectron – S. cervesiae

In this example the existence of the T1-T2 (5515-5533) long loop is controlled by a C1/C2 short loop (6102). The expression of this C1/C2 short loop is controlled only by the gene YNL339C.



A double stranded DNA loop of length 6.466 kilo-bases on chromosome 12 is bounded on the left by a T1 sequence whose identifier is 5515. This T1 control element has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 5533. This T2 control element has the DNA sequence

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

YLR467W

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 14 whose identifier is 6102 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YNL339C and has the DNA sequence

AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTGAACATCCGGGTAAGAGACAACAGGGCT

The match between the T1 sequence and the C1/C2 sequence is

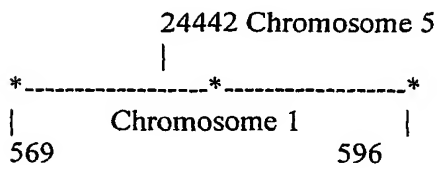
AGGAAATTGTTGTTACGAAAGTCAGTGATTATGTATTGTGTAGTATAGTAT
ATTGTAAGAAATTTTTTTTTCTAGGGAATATGCGTTTTGATGTAGTAGTAT
TTCACTGTTTTGATTTAGTGTTTGTTGCACGGCAGTAGCGAGAGACAAGTG
GGAAAGAGTAGGATAAAAAGACAATCTATAAAAAGTAAACATAAAATAA
AGGTAGTAAGTAGCTTTTGGTTG

The match between the T2 sequence and the C1/C2 sequence is

ATTATGTATTGTGTAGTATAGTATATTGTAAGAAATTTTTTTTTCTAGGGA
ATATGCGTTTTGATGTAGTAGTATTTCACTGTTTTGATTTAGTGTTTGTTGC
ACGGCAGTAGCGAGAGACAAGTGGGAAAGAGTAGGATAAAAAGACAATC
TATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGGTTGAACA
TCCGGGTAAGAGACAACAGGGCT

Example of a multi-celled permanent connectron – C. elegans

In this example the existence of the T1-T2 (5515-5533) long loop is controlled by a C1/C2 short loop (6102). The expression of this C1/C2 short loop is controlled only by the gene YNL339C.



A double stranded DNA loop of length 30.606 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 569. This T1 control element has the DNA sequence

AAATCGAGCCCGTAAATCGACACAAGCGCTACAGTAGTC

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 596. This T2 control element has the DNA sequence

AGTGCTACAGTAGTCATTTAAAGAATTACTGTAGTTTTCGCT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 5 whose identifier is 24442 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene F20D6.4 and has the DNA sequence

GAGCCCGTAAATCGACACAAGCGCTACAGTAGTCATTTAAAGAATTACTG
TAGTTTTC

The match between the T1 sequence and the C1/C2 sequence is

GAGCCCGTAAATCGACACAAGCGCTACAGTAGTC

The match between the T2 sequence and the C1/C2 sequence is

5

GCTACAGTAGTCATTTAAAGAATTACTGTAGTTTTC

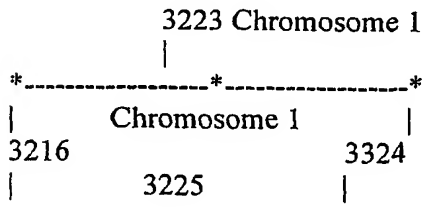
---

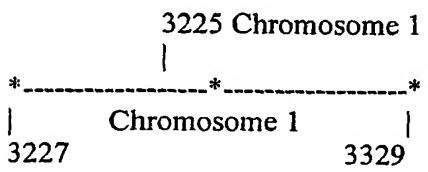
7. Transient connectrons exist in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

A class of connectron relationships exist that permit one C1/C2 short loop to control the existence of one or more T1-T2 long loops such that this C1/C2 short loop is itself subject to expression control by another T1-T2 long loop which surrounds it. These connectron relationships are described as "transient". Transient connectrons exist in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

Example of a prokaryote transient connectron – E. coli

In this example the existence of the T1-T2 (3227-3329) long loop is controlled by the C1/C2 (3225) short loop. The expression of this C1/C2 short loop is controlled by the existence of the T1-T2 (3216-3224) long loop. The existence of this T1-T2 long loop is itself determined by the expression of the C1/C2 (3223) short loop. The C1/C2 (3225) short loop is the transient connectron.





A double stranded DNA loop of length 93.464 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3216. This T1 control element has the DNA sequence

AGCGCAAGCGAAGCTCTTGATCGAAGCCCCGGTAAACGGCGGCCGTAACT
ATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGACCTGC
ACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCGAGACTCAGTGAAA
TTGAACTCGCTGTGAAGATGCAGTGTACCCGCGGCAAGACGGAAAGACCC
CGTGAACCTTTACTATAGCTTGACACTGAACATTGAGCCTTGATGTGTAGG
ATAGGTGGGAGGCTTTGAAGTGTGGACGCCAGTCTGCATGGAGCCGACCT
TGAAATACCACCCTTTAATGTTTGATGTTCTAACGT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3324. This T2 control element has the DNA sequence

CCCGGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCC
TTGTCGGGTAAGTTCCGACCTGCACGAATGGCGTAATGATGGCCAGGCTG
TCTCCACCCGAGACTCAGTGAAATTGAACTCGCTGTGAAGATGCAGTGTA
CCCGCGGCAAGACGGAAAGACCCCGTGAACCTTTACTATAGCTTGACACT
GAACATTGAGCCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGTGTGGA
CGCCAGTCTGCATGGAGCCGACCTTGAAATACCACCCTTTAATGTTTGATG
TTCTAACGTTGACCCGTAATCCGGGTTGCGGACAGT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

rrfC aspT trpT yifA yifE yifB ilvL ilvG_1 ilvM
ilvE ilvD ilvA ilvY ilvC ppiC b3776 rep gppA
rhlB trxA rhoL rho rfe wzzE wecB rffH wecD
wecE wzxE yifM_2 wecG yifK argX hisR leuT
proM aslB aslA hemY hemX hemD cyaA cyaY
b3808 dapF uvrD b3814 corA yigF yigG rarD yigI
pldA recQ yigJ yigK pldB yigL yigM metR metE
ysgA udp yigN ubiE yigP b3836 yigU yigW_1 rfaH
yigC ubiB fadA fadB pepQ trkH hemG rrsA ileT
rrlA

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 3225 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrlC and has the DNA sequence

AAACAGAATTTGCCTGGCGGCCGTAGCGCGGTGGTCCCACCTGACCCCAT
GCCGAACTCAGAAGTGAAACGCCGTAGCGCCGATGGTAGTGTGGGGTCTC
CCCATGCGAGAGTAGGGAACTGCCAGGCATCAAATTA

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 3323 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrlA and has the DNA sequence

GCGAAGCTCTTGATCGAAGCCCCGGTAAACGGCGGCCGTAACTATAACGG
TCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGACCTGCACGAATG
GCGTAATGATGGCCAGGCTGTCTCCACCCGAGACTCAGTGAAATTGAACT
CGCTGTGAAGATGCAGTGTACCCGCGGCAAGACGGA...AACAGAATTTGC
CTGGCGGCAGTAGCGCGGTGGTCCCACCTGACCCCATGCCGAACTCAGAA
GTGAAACGCCGTAGCGCCGATGGTAGTGTGGGGTCTC

The match between the T1 sequence and the C1/C2 sequence is

GCGAAGCTCTTGATCGAAGCCCCGGTAAACGGCGGCCGTAACTATAACGG
TCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGACCTGCACGAATG
GCGTAATGATGGCCAGGCTGTCTCCACCCGAGACTCAGTGAAATTGAACT

CGCTGTGAAGATGCAGTGTACCCGCGGCAAGACGGAAAGACCCCGTGAA
CCTTTACTATAGCTTGACACTGAACATTGAGCCTTGATGTGTAGGATAGGT
GGGAGGCTTTGAAGTGTGGACGCCAGTCTGCATGGAGCCGACCTTGAAAT
ACCACCCTTTAATGTTTGATGTTCTAACGT

The match between the T2 sequence and the C1/C2 sequence is

CCCGGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCC
TTGTCGGGTAAGTTCCGACCTGCACGAATGGCGTAATGATGGCCAGGCTG
TCTCCACCCGAGACTCAGTGAAATTGAACTCGCTGTGAAGATGCAGTGTA
CCCGCGGCAAGACGGAAAGACCCCGTGAACCTTTACTATAGCTTGACACT
GAACATTGAGCCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGTGTGGA
CGCCAGTCTGCATGGAGCCGACCTTGAAATACCACCCTTTAATGTTTGATG
TTCTAACGTTGACCCGTAATCCGGGTTGCGGACAGT

A double stranded DNA loop of length 93.749 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3227. This T1 control element has the DNA sequence

AGCGCCGATGGTAGTGTGGGGTCTCCCCATGCGAGAGTAGGGAACTGCCA
GG

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3329. This T2 control element has the DNA sequence

CATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAG
TCG

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

aspT trpT yifA yifE yifB ilvL ilvG_1 ilvM ilvE
ilvD ilvA ilvY ilvC ppiC b3776 rep gppA rhlB
trxA rhoL rho rfe wzzE wecB rffH wecD wecE
wzxE yifM_2 wecG yifK argX hisR leuT proM
aslB aslA hemY hemX hemD cyaA cyaY b3808
dapF uvrD b3814 corA yigF yigG rarD yigI pldA
recQ yigJ yigK pldB yigL yigM metR metE ysgA
udp yigN ubiE yigP b3836 yigU yigW_1 rfaH yigC
ubiB fadA fadB pepQ trkH hemG rrsA ileT rrlA
rrfA

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 3225 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene rrlC and has the DNA sequence

AAACAGAATTTGCCTGGCGGCCGTAGCGCGGTGGTCCCACCTGACCCCAT
GCCGAACTCAGAAGTGAAACGCCGTAGCGCCGATGGTAGTGTGGGGTCTC
CCCATGCGAGAGTAGGGAACTGCCAGGCATCAAATTA

The match between the T1 sequence and the C1/C2 sequence is

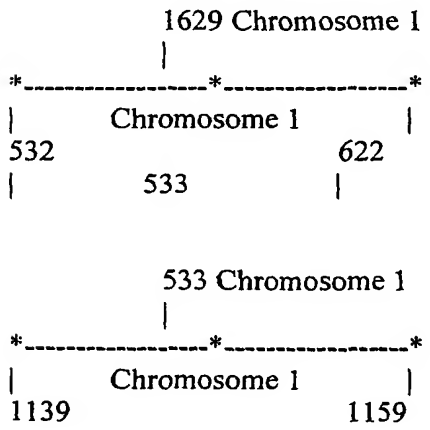
AGCGCCGATGGTAGTGTGGGGTCTCCCCATGCGAGAGTAGGGAACTGCCA
GG

The match between the T2 sequence and the C1/C2 sequence is

CATGCGAGAGTAGGGAACTGCCAGGCATCAAAT

Example of an archea transient connectron – M. jannaschii

In this example the existence of the T1-T2 (1139-1159) long loop is controlled by the C1/C2 (533) short loop. The expression of this C1/C2 short loop is controlled by the existence of the T1-T2 (532-622) long loop. The existence of this T1-T2 long loop is itself determined by the expression of the C1/C2 (1629) short loop. The C1/C2 (533) short loop is the transient connectron.



A double stranded DNA loop of length 78.672 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 532. This T1 control element has the DNA sequence

ATATGTTTGAAATTTGAAAATAAGAGTATTTAG

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 622. This T2 control element has the DNA sequence

TTGAAAATAAGAGCATTTAGAAGTTATTAATTAGTTCAAAGGATTTT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

MJ0486	MJ0487	MJ0488	MJ0489	MJ0490	MJ0492	MJ0493
MJ0494	MJ0495	MJ0496	MJ0497	MJ0499	MJ0500	MJ0501
MJ0502	MJ0503	MJ0504	MJ0506	MJ0507	MJ0508	MJ0509
MJ0510	MJ0511	MJ0512	MJ0513	MJ0514	MJ0514	MJ0517
MJ0519	MJ0520	MJ0521	MJ0522	MJ0523	MJ0525	MJ0526
MJ0526	MJ0529	MJ0530	MJ0531	MJ0532	MJ0534	MJ0535
MJ0536	MJ0538	MJ0539	MJ0540	MJ0541	MJ0542	MJ0543
MJ0544	MJ0545	MJ0547	MJ0548	MJ0549	MJ0550	MJ0552
MJ0553	MJ0554	MJ0555	MJ0556	MJ0557	MJ0558	MJ0559
MJ0560	MJ0561	MJ0562	MJ0563	MJ0564	MJ0565	MJ0566
MJ0568	MJ0569	MJ0570				

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 533 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ0485 and has the DNA sequence

ATTTTTATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGA GTTTATTGAATT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 1629 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1597 and has the DNA sequence

ATATGTTTGAAATTTGAAAATAAGAGTATTTAGAAGTTATTAATTAGTTCA
AAGGATTTTTATTTAATTTCTAAGGGTTTGCTGGTTTGATTATTTAGAATAT
TTGAGTTTATTGAATTATTCAGATTTTTAAAAATTA

The match between the T1 sequence and the C1/C2 sequence is

ATATGTTTGAAATTTGAAAATAAGAGTATTTAG

The match between the T2 sequence and the C1/C2 sequence is

ATTTAGAAGTTATTAATTAGTTCAAAGGATTTT

A double stranded DNA loop of length 14.509 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 1139. This T1 control element has the DNA sequence

ATTTATTAATTAGTTCAAAGGATTTTTATTTAATTTCTAAGGGTTAGCTGG
TTTGATTGTTTAAAATATTTGAGTTTA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1159. This T2 control element has the DNA sequence

ATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATTATTCAGATTTTTAAAAATTA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

MJ1096 MJ1097 tRNA-Arg-3 MJ1098 MJ1099 MJ1100 MJ1101
MJ1102 MJ1103 MJ1104 MJ1105 MJ1106 MJ1107 MJ1108

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 533 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ0485 and has the DNA sequence

ATTTTTATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGA
GTTTATTGAATT

The match between the T1 sequence and the C1/C2 sequence is

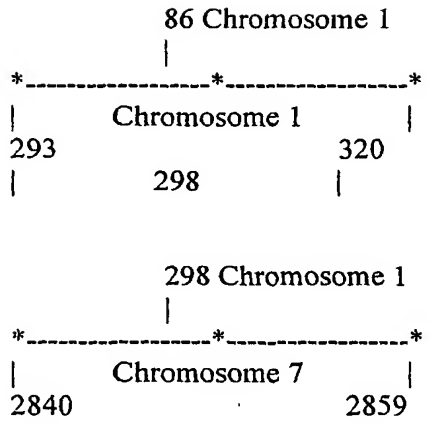
ATTTTTATTTAATTTCTAAGGGTTAGCTGGTTTGATT

The match between the T2 sequence and the C1/C2 sequence is

ATTTAATTTCTAAGGGTTAGCTGGTTTGATTATTTAGAATATTTGAGTTTAT
TGAATT

Example of a single-celled transient connectron – S. cervesiae

In this example the existence of the T1-T2 (2840-2859) long loop is controlled by the C1/C2 (298) short loop. The expression of this C1/C2 short loop is controlled by the existence of the T1-T2 (293-320) long loop. The existence of this T1-T2 long loop is itself determined by the expression of the C1/C2 (86) short loop. The C1/C2 (298) short loop is the transient connectron.



A double stranded DNA loop of length 38.470 kilo-bases on chromosome 2 is bounded on the left by a T1 sequence whose identifier is 293. This T1 control element has the DNA sequence

GAATTGTTGGAATAAAAATCCACTATCGTCTATCAACTAATAGTTATATTA
TCAATATATTATCATATACGGTGTTAAGATGATGACATAAGTTATGAGAA
GCTGTCATCGAAGTTAGAGGAAGCTGAAGTGCAAGGATTGATAATGTAAT
AGGATAATGAAACATATAAAACGGAATGAGGAATAATCGTAATATTAGT
ATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTTGAGGAGAAC
TTCTAGT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 320. This T2 control element has the DNA sequence

AATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTC
GAGGAGAACTTCTAGTATATTCTGTA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

YBL005W-B TS(AGA)B YBL004W YBL003C YBL002W YBL001C YBR001C YBR002C YBR003W YBR004C YBR005W YBR006W YBR007C YBR008C YBR009C YBR010W YBR011C YBR012C

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 2 whose identifier is 298 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YBL005W-B and has the DNA sequence

ATCTATTACATTATGGGTGGTATGTTGGAATAAAAATCCACTATCGTCTAT
CAACTAATAGTTATATTATCAATATATTATCATATACGGTGTTAAGATGAT
GACATAAGTTATGAGAAGCTGTCATCGAAGTTAGAGGAAGCTGAAGTGCA
AGGATTGATAATGTAATAGGATAATGAAACATATAAAACGGAATGAGGA
ATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCT
ATATCCTTGAGGAGAACTTCTAGTATATTCTGTATACCTAATATTATAGCC
TTTATCAACAATGGAATCCCAACAATTATCTCAACATTC

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 86 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YAR009C and has the DNA sequence

ATCTATTACATTATGGGTGGTATGTTGGAATAGAAATCAACTATCATCTAC
TAACTAGTATTTACATTACTAGTATATTATCATATACGGTGTTAGAAGATG
ACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCTGAAACGCA
AGGATTGATAATGTAATAGGATCAATGAATATAAACATATAAAACGGAAT

GAGGAATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGAGG
ATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTAATATT
ATAGCCTTTATCAACAATGGAATCCCAACAATTATCTCAACATTCACCCAT
TTCTCAGAA

The match between the T1 sequence and the C1/C2 sequence is

AAACATATAAAACGGAATGAGGAATAATCGTAATATTAGTATGTAGAAAT
ATAGATTCCATTTTGAGGATTCCTATATCCT

The match between the T2 sequence and the C1/C2 sequence is

AATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTC
GAGGAGAACTTCTAGTATATTCTGTA

A double stranded DNA loop of length 5.302 kilo-bases on chromosome 7 is bounded on the left by a T1 sequence whose identifier is 2840. This T1 control element has the DNA sequence

TCTGTTGGAATAAAAATCCACTATCGTCTATCAACTAATAGTTATATTATC
AATATATTATCATATACGGTGTTAAGATGATGACATAAGTTATGAGAAGC
TGTCATCGAAGTTAGAGGAAGCTGAAACGCAAGGATTGATAATGTAATAG
GATCAATGAATATAAACATATAAAACGGAATGAGGAATAATCGTAATATT
AGTATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTCGAGGAG
AACTTCTAGTATATTCTGTATACCTAAATTATAGCCTTTATCAACAATGGA
ATCCCAACAA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 2859. This T2 control element has the DNA sequence

CTATCAACTAATAGTTATATTATCAATATATTATCATATACGGTGTTAAGA
TGATGACATAAGTTATGAGAAGCTGTCATCGAAGTTAGAGGAAGCTGAAA
CGCAAGGATTGATAATGTAATAGGATCAATGAATATAAACATATAAAACG
GAATGAGGAATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTT
GAGGATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTAA
TATTATAGCCTTTATCAACAATGGAATCCCAACAATTATCTCAACATTCAC
ATATTTCTCAT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 2 whose identifier is 298 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YBL005W-B and has the DNA sequence

ATCTATTACATTATGGGTGGTATGTTGGAATAAAAATCCACTATCGTCTAT
CAACTAATAGTTATATTATCAATATATTATCATATACGGTGTTAAGATGAT
GACATAAGTTATGAGAAGCTGTCATCGAAGTTAGAGGAAGCTGAAGTGCA
AGGATTGATAATGTAATAGGATAATGAAACATATAAAACGGAATGAGGA
ATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCT
ATATCCTTGAGGAGAACTTCTAGTATATTCTGTATACCTAATATTATAGCC
TTTATCAACAATGGAATCCCAACAATTATCTCAACATTC

The match between the T1 sequence and the C1/C2 sequence is

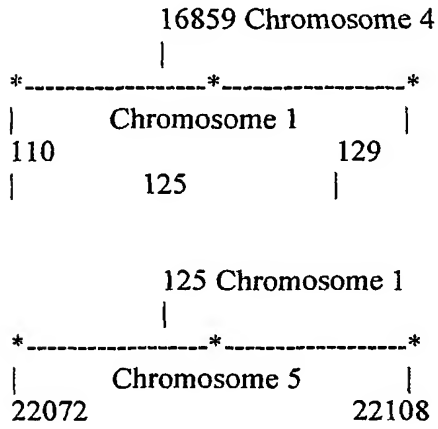
TGTTGGAATAAAAATCCACTATCGTCTATCAACTAATAGTTATATTATCAA
TATATTATCATATACGGTGTTAAGATGATGACATAAGTTATGAGAAGCTG
TCATCGAAGTTAGAGGAAGCTGAA

The match between the T2 sequence and the C1/C2 sequence is

CTATCAACTAATAGTTATATTATCAATATATTATCATATACGGTGTTAAGA
TGATGACATAAGTTATGAGAAGCTGTCATCGAAGTTAGAGGAAGCTGAA

Example of a multi-celled transient connectron – C. elegans

In this example the existence of the T1-T2 (22072-22108) long loop is controlled by the C1/C2 (125) short loop. The expression of this C1/C2 short loop is controlled by the existence of the T1-T2 (110-129) long loop. The existence of this T1-T2 long loop is itself determined by the expression of the C1/C2 (16859) short loop. The C1/C2 (125) short loop is the transient connectron.



A double stranded DNA loop of length 18.855 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 110. This T1 control element has the DNA sequence

AGCTTAGGCTTAAGCTTAGGCTTAAGCTTAGGC

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 129. This T2 control element has the DNA sequence

TTCTCCCGCATTTTTTGTAGATCTACGTAGATCAAACCGAAATGAGGCACT
TTCTGAATCCACGAGCTAGGCTTAAGCTTAGGCTTAAGCTTAGGCCTTTTC
TCAGGCTTAGGCTTAGGCTTA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

ZC123.3 ZC123.2

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 125 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZC123.3 and has the DNA sequence

ACGCGCCGTAAATCTACCCCAGATATGGCCGAGCCAAAATGGCCTAGTTC
GGCAAACTCTTTCATTTCAATTTATGAGGGAAGCCAGAA

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 4 whose identifier is 16859 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene F58E2.7 and has the DNA sequence

CTTAGGCTTAAGCTTAGGCTTAAGCTTAGGCTTAAGCTTAGGCTTAAGCTT
AGGCTTAAGCTTAGGCTTAAGCTTAGGCTTAAGCTTAGGCTTAAGCTTAG
GCTTAAGCTTAGGCTTAAGCTTAGGCTTAAGCTTAGGCTTAAGCTTAGGCT
TAAGCTTAGACTTA

The match between the T1 sequence and the C1/C2 sequence is

AGCTTAGGCTTAAGCTTAGGCTTAAGCTTAGGC

The match between the T2 sequence and the C1/C2 sequence is

TAGGCTTAAGCTTAGGCTTAAGCTTAGGC

A double stranded DNA loop of length 51.031 kilo-bases on chromosome 5 is bounded on the left by a T1 sequence whose identifier is 22072. This T1 control element has the DNA sequence

CGCAACGCGCCGTAAATCTACCCCAGATATGGCCGAGCCAAAATGACCTA
GTTCGGC

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 22108. This T2 control element has the DNA sequence

TGACAATCGCCTGCCGGACAACGCGTGGAAAAGTGTCGTGTACTCCACAC
GGACAAATACATTTAGTTTTACAACTAAAATCGAACCGCGACGCGACACG
CAACGCGACGTAAATCTACCCCAGATATGGCCGAGCCAAAATGGCCTAGT
TCGGCAAACTCTTCTATTTC

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

F36H9.3 F36H9.4 F36H9.5 F36H9.2 F36H9.1 F36H9.6

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 125 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZC123.3 and has the DNA sequence

ACGCGCCGTAAATCTACCCCAGATATGGCCGAGCCAAAATGGCCTAGTTC
GGCAAACTCTTTCATTTCAATTTATGAGGGAAGCCAGAA

The match between the T1 sequence and the C1/C2 sequence is

ACGCGCCGTAAATCTACCCCAGATATGGCCGAGCCAAAATG

The match between the T2 sequence and the C1/C2 sequence is

CGTAAATCTACCCCAGATATGGCCGAGCCAAAATGGCCTAGTTCGGCAAA
CTCTT

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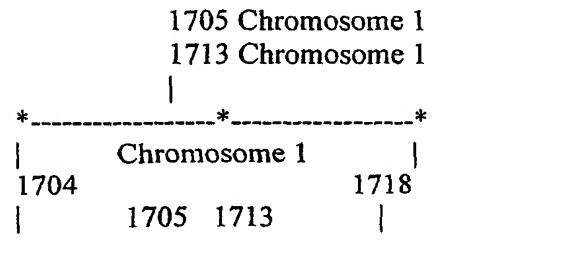
8. Self-limiting connectrons occur in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes

A class of connectron relationships exist that permit one C1/C2 short loop to control the existence of the T1-T2 long loop that surrounds it. These connectron relationships are described as "self-limiting". Self-limiting connectrons exist in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes.

Example of a prokaryotic self-limiting connectrons – E. coli

In this example the existence of the T1-T2 (1704-1718) long loop is controlled by two C1/C2 (1705 and 1713) short loops. The expression of these C1/C2 short loops is controlled by the existence of the T1-T2 (1704-1718) long loop. The existence of this T1-T2 long loop is itself determined by the expression of the two C1/C2 (1705 and 1713) short loops. The C1/C2 (1705 and 1713) short loops are the self-limiting connectrons.



A double stranded DNA loop of length 15.259 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 1704. This T1 control element has the DNA sequence

CGCCCCGTTCACACGATTCCTCTGTAGTTCAGTCGGTAGAACGGCGGACT
GTTAATCCGTATGTCACTGGT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1718. This T2 control element has the DNA sequence

TTCAGTCGGTAGAACGGCGGACTGTTAATCCGTATGTCACTGGTTCGAGTC
CAGTCAGAGGAGCCAAATTC

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

asnT b1978 b1979 b1980 shiA amn b1983 asnW yeeO asnU

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 1705 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene and has the DNA sequence

CGCCCCGTTCACACGATTCCTCTGTAGTTCAGTCGGTAGAACGGCGGACT
GTTAATCCGTATGTCACTGGTTCGAGTCCAGTCAGAGGAGCCAAATTC

A C1/C2 short loop on chromosome 1 whose identifier is 1713 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene asnW and has the DNA sequence

CACGATTCCTCTGTAGTTCAGTCGGTAGAACGGCGGACTGTTAATCCGTAT
GTCACTGGTTCGAGTCCAGTCAGAGGAGCCAAATT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 1705 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene and has the DNA sequence

CGCCCCGTTCACACGATTCCTCTGTAGTTCAGTCGGTAGAACGGCGGACT
GTTAATCCGTATGTCACTGGTTCGAGTCCAGTCAGAGGAGCCAAATTC

The match between the T1 sequence and the C1/C2 sequence is

CGCCCCGTTCACACGATTCCTCTGTAGTTCAGTCGGTAGAACGGCGGACT
GTTAATCCGTATGTCACTGGT

The match between the T2 sequence and the C1/C2 sequence is

TTCAGTCGGTAGAACGGCGGACTGTTAATCCGTATGTCACTGGTTCGAGTC
CAGTCAGAGGAGCCAAATTC

A C1/C2 short loop on chromosome 1 whose identifier is 1713 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene asnW and has the DNA sequence

CACGATTCCTCTGTAGTTCAGTCGGTAGAACGGCGGACTGTTAATCCGTAT
GTCACTGGTTCGAGTCCAGTCAGAGGAGCCAAATT

The match between the T1 sequence and the C1/C2 sequence is

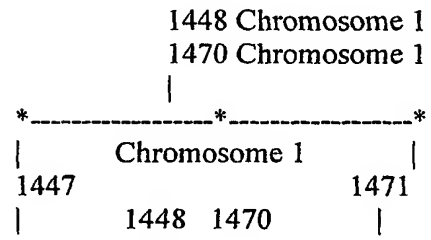
CACGATTCCTCTGTAGTTCAGTCGGTAGAACGGCGGACTGTTAATCCGTAT
GTCACTGGT

The match between the T2 sequence and the C1/C2 sequence is

TTCAGTCGGTAGAACGGCGGACTGTTAATCCGTATGTCACTGGTTCGAGTC
CAGTCAGAGGAGCCAAATT

Example of a archea self-limiting connectrons – M. jannaschii

In this example the existence of the T1-T2 (1447-1471) long loop is controlled by two C1/C2 (1448 and 1470) short loops. The expression of these C1/C2 short loops is controlled by the existence of the T1-T2 (1447-1471) long loop. The existence of this T1-T2 long loop is itself determined by the expression of the two C1/C2 (1705 and 1713) short loops. The C1/C2 (1448 and 1470) short loops are the self-limiting connectrons.



A double stranded DNA loop of length 22.675 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 1447. This T1 control element has the DNA sequence

TTATAGAACATTATGAAGCTTTTTACTCAACTAACAACCGTATCGAATTTA
CCATTACTTGGAAATCTATTTAAAACCTCTTTAATCTTATGATA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1471. This T2 control element has the DNA sequence

CAACTAACAACCGTATCGAATTTACCATTACTTGGAAATCTATTTAAAACC
TCTTTAATCTTGTGATAATAAATTCTAATCGATTCGTGACTTAT

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

MJ1402 MJ1403 MJ1404 MJ1405 MJ1406 MJ1407 MJ1408
MJ1409 MJ1410 MJ1411 MJ1412 MJ1413 MJ1414 MJ1415
MJ1416 MJ1417 MJ1418 MJ1419 MJ1420

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 1448 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1401 and has the DNA sequence

TTATAGAACATTATGAAGCTTTTTACTCAACTAACAACCGTATCGAATTTA
CCATTACTTGGAAATCTATTTAAAACCTCTTTAATCTTATGATAATAAATT
CTAATCGATTCGTGACTTAT

A C1/C2 short loop on chromosome 1 whose identifier is 1470 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1420 and has the DNA sequence

TTATAGAACATTATGAAGCTTTTTACTCAACTAACAACCGTATCGAATTTA
CCATTACTTGGAAATCTATTTAAAACCTCTTTAATCTTGTGATAATAAATT
CTAATCGATTCGTG

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 1470 controls the expression of the genes in this T1/T2 long loop.This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1420 and has the DNA sequence

TTATAGAACATTATGAAGCTTTTTACTCAACTAACAACCGTATCGAATTTA
CCATTACTTGGAAATCTATTTAAAACCTCTTTAATCTTGTGATAATAAATT
CTAATCGATTCGTG

The match between the T1 sequence and the C1/C2 sequence is

TTATAGAACATTATGAAGCTTTTTACTCAACTAACAACCGTATCGAATTTA
CCATTACTTGGAAATCTATTTAAAACCTCTTTAATCTT

The match between the T2 sequence and the C1/C2 sequence is

CAACTAACAACCGTATCGAATTTACCATTACTTGGAAATCTATTTAAAACC
TCTTTAATCTTGTGATAATAAATTCTAATCGATTCGTG

A C1/C2 short loop on chromosome 1 whose identifier is 1448 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene MJ1401 and has the DNA sequence

TTATAGAACATTATGAAGCTTTTTACTCAACTAACAACCGTATCGAATTTA
CCATTACTTGGAAATCTATTTAAAACCTCTTTAATCTTATGATAATAAATT
CTAATCGATTCGTGACTTAT

The match between the T1 sequence and the C1/C2 sequence is

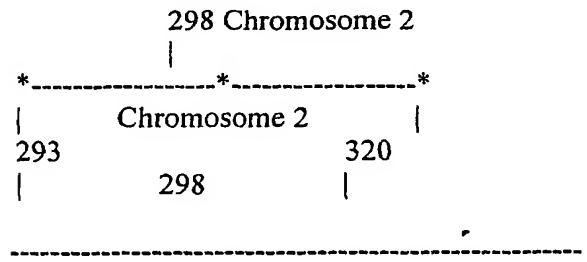
TTATAGAACATTATGAAGCTTTTTACTCAACTAACAACCGTATCGAATTTA
CCATTACTTGGAAATCTATTTAAAACCTCTTTAATCTTATGATA

The match between the T2 sequence and the C1/C2 sequence is

CAACTAACAACCGTATCGAATTTACCATTACTTGGAAATCTATTTAAAACC
TCTTTAATCTT

Example of a single-celled self-limiting connectron – S. cervesiae

In this example the existence of the T1-T2 (293-320) long loop is controlled by C1/C2 (298) short loop. The expression of this C1/C2 short loop is controlled by the existence of the T1-T2 (293-320) long loop. The existence of this T1-T2 long loop is itself determined by the expression of the C1/C2 (298) short loop. The C1/C2 (298) short loop is the self-limiting connectron.



A double stranded DNA loop of length 38.470 kilo-bases on chromosome 2 is bounded on the left by a T1 sequence whose identifier is 293. This T1 control element has the DNA sequence

GAATTGTTGGAATAAAAATCCACTATCGTCTATCAACTAATAGTTATATTA
TCAATATATTATCATATACGGTGTTAAGATGATGACATAAGTTATGAGAA
GCTGTCATCGAAGTTAGAGGAAGCTGAAGTGCAAGGATTGATAATGTAAT

AGGATAATGAAACATATAAAACGGAATGAGGAATAATCGTAATATTAGT
ATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTTGAGGAGAAC
TTCTAGT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 320. This T2 control element has the DNA sequence

AATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCTC
GAGGAGAACTTCTAGTATATTCTGTA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

YBL005W-B TS(AGA)B YBL004W YBL003C YBL002W YBL001C
YBR001C YBR002C YBR003W YBR004C YBR005W YBR006W
YBR007C YBR008C YBR009C YBR010W YBR011C YBR012C

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 2 whose identifier is 298 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YBL005W-B and has the DNA sequence

ATCTATTACATTATGGGTGGTATGTTGGAATAAAAATCCACTATCGTCTAT
CAACTAATAGTTATATTATCAATATATTATCATATACGGTGTTAAGATGAT
GACATAAGTTATGAGAAGCTGTCATCGAAGTTAGAGGAAGCTGAAGTGCA
AGGATTGATAATGTAATAGGATAATGAAACATATAAAACGGAATGAGGA
ATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCT
ATATCCTTGAGGAGAACTTCTAGTATATTCTGTATACCTAATATTATAGCC
TTTATCAACAATGGAATCCCAACAATTATCTCAACATTC

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 2 whose identifier is 298 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YBL005W-B and has the DNA sequence

ATCTATTACATTATGGGTGGTATGTTGGAATAAAAATCCACTATCGTCTAT
CAACTAATAGTTATATTATCAATATATTATCATATACGGTGTTAAGATGAT
GACATAAGTTATGAGAAGCTGTCATCGAAGTTAGAGGAAGCTGAAGTGCA
AGGATTGATAATGTAATAGGATAATGAAACATATAAAACGGAATGAGGA
ATAATCGTAATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCT
ATATCCTTGAGGAGAACTTCTAGTATATTCTGTATACCTAATATTATAGCC
TTTATCAACAATGGAATCCCAACAATTATCTCAACATTC

The match between the T1 sequence and the C1/C2 sequence is

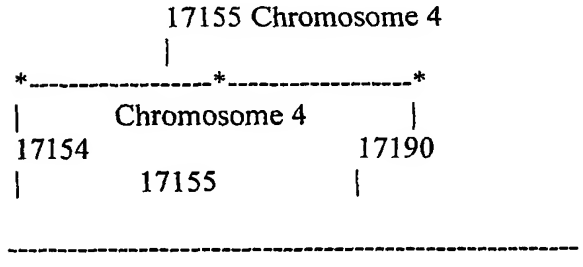
TGTTGGAATAAAAATCCACTATCGTCTATCAACTAATAGTTATATTATCAA
TATATTATCATATACGGTGTTAAGATGATGACATAAGTTATGAGAAGCTG
TCATCGAAGTTAGAGGAAGCTGAAGTGCAAGGATTGATAATGTAATAGGA
TAATGAAACATATAAAACGGAATGAGGAATAATCGTAATATTAGTATGTA
GAAATATAGATTCCATTTTGAGGATTCCTATATCCTTGAGGAGAACTTCTA
GT

The match between the T2 sequence and the C1/C2 sequence is

AATATTAGTATGTAGAAATATAGATTCCATTTTGAGGATTCCTATATCCT

Example of a multi-celled self-limiting connectron – C. elegans

In this example the existence of the T1-T2 (293-320) long loop is controlled by C1/C2 (298) short loop. The expression of this C1/C2 short loop is controlled by the existence of the T1-T2 (293-320) long loop. The existence of this T1-T2 long loop is itself determined by the expression of the C1/C2 (298) short loop. The C1/C2 (298) short loop is the self-limiting connectron.



A double stranded DNA loop of length 89.919 kilo-bases on chromosome 4 is bounded on the left by a T1 sequence whose identifier is 17154. This T1 control element has the DNA sequence

AAATTTCCGGCAAATCGGCAAACTGGCAA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 17190. This T2 control element has the DNA sequence

AATTTGCCGATTTGCCGAATTTGTCGACA

This long T1/T2 double stranded DNA loop modulates the expression of the following genes

R08C7.11 M01H9.2 M01H9.3 M01H9.4 M01H9.1 ZK180.1 ZK180.2 ZK180.3 ZK180.4 ZK180.5 ZK180.6 ZK185.3 ZK185.2

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 4 whose identifier is 17155 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene R08C7.1 and has the DNA sequence

AAATTTCCGGCAAATCGGCAAACTGGCAATTTGCCGATTTGCCGAATTTGT
CGACA

A C1/C2 short loop on chromosome 4 whose identifier is 17171 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene ZK180.2 and has the DNA sequence

TGGAAATTTCAGAATTTCAATTTTAATCGGCAAAATTGTACGCATCCTATG
AATTT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 4 whose identifier is 17155 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene R08C7.1 and has the DNA sequence

AAATTTCCGGCAAATCGGCAAACTGGCAATTTGCCGATTTGCCGAATTTGT
CGACA

The match between the T1 sequence and the C1/C2 sequence is

AAATTTCCGGCAAATCGGCAAACTGGCAA

The match between the T2 sequence and the C1/C2 sequence is

AATTTGCCGATTTGCCGAATTTGTCGACA

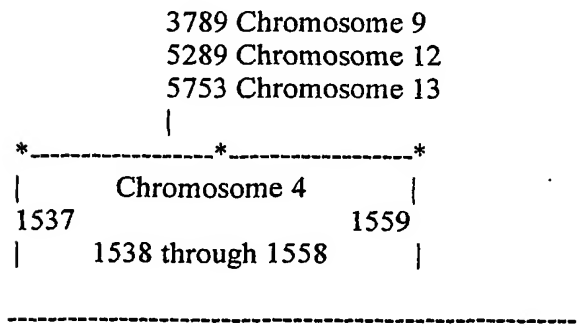
5

9. Geneless connectrons exist in single-celled and multi-celled eukaryotes

Normally T1-T2 long loops contain genes whose expression is regulated by the existence of the long loop. When a T1-T2 long loop does not contain any genes it is described as being "geneless". The existence of the T1-T2 long loop is itself controlled by one or more C1/C2 short loops that may be on the same or different chromosomes. The geneless T1-T2 long loops must contain one or more C1/C2 short loops.

Example of a single-celled geneless connectron – S. cervesiae

In this example the existence of the T1-T2 (1537-1559) long loop is controlled by three C1/C2 (3789, 5289 and 5753) short loops. The expression of 21 C1/C2 (1538 through 1558) short loops are controlled by the existence of the T1-T2 (1537-1559) long loop.



A double stranded DNA loop of length 4.825 kilo-bases on chromosome 4 is bounded on the left by a T1 sequence whose identifier is 1537. This T1 control element has the DNA sequence

ATGAGATATATGTGGGTAATTAGATAATTGTTGGGATTCCATTGTTGATAA
AGGCTATAATATTAGGTATACAGAATATACTAGAAGTTCTCCTCGAGGAT
TTAGGAATCCATAAAAGGGAATCTGCAATTCTACACAATTCTATAAATAT
TATTATCATCGTTTTATATGTTAATATTCATTGATCCTATTACATTATCAAT

CCTTGCGTTTCAGCTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGT
CATCTTCTAACACCGTATATGATAATATACTAGTAACGTAAATACTAGTTA
GTAGATGATAGTTGATTTTTATTCCAACATACCACCCATAATGTAATAGAT
CTAAT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1559. This T2 control element has the DNA sequence

ATGAGATATATGTGGGTAATTAGATAATTGTTGGGATTCCATTGTTGATAA
AGGCTATAATATTAGGTATACAGAATATACTAGAAGTTCTCCTCGAGGAT
TTAGGAATCCATAAAAGGGAATCTGCAATTCTACACAATTCTATAAATAT
TATTATCATCGTTTTATATGTTAATATTCATTGATCCTATTACATTATCAAT
CCTTGCGTTTCAGCTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGT
CATCTTCTAACACCGTATATGATAATATACTAGTAACGTAAATACTAGTTA
GTAGATGATAGTTGATTTTTATTCCAACATACCACCCATAATGTAATAGAT
CTAAT

There are no genes controlled by this T1/T2 loop.

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 4 whose identifier is 1538 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

ATGAGATATATGTGGGTAATTAGATAATTGTTGGGATTCCATTGTTGATAA
AGGCTATAATATTAGGTATACAGAATATACTAGAAGTTCTCCTCGAGGAT
TTAGGAATCCATAAAAGGGAATCTGCAATTCTACACAATTCTATAAATAT
TATTATCATCGTTTTATATGTTAATATTCATTGATCCTATTACATTATCAAT
CCTTGCGTTTCAGCTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGT
CATCTTCTAACACCGTATATGATAATATACTAGTAACGTAAATACTAGTTA

GTAGATGATAGTTGATTTTTATTCCAACATACCACCCATAATGTAATAGAT
CTAATGAATCCATTTGTTTGTTAATAGTTT

This T1-T2 loop also modulates the C1/C2 short loops numbered 1539 to 1557

A C1/C2 short loop on chromosome 4 whose identifier is 1558 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

AGCTTCTCATAACTTATGTCATCATCTTAACACCGTATATGATAATATATT
GATAATATAACTTGTTGGAATAAAAATCAACTATCATCTACTAACTAGTAT
TTACGTTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATG
ATGAGAAATAGTCATCTAAATTAGTGGAAGCTGA...GTCTATCTGGCGAAT
ATAAATTTTTACGCTACACACGTCATCGACATCTAAATATGACAGTCGCTG
AACTGTTCTTAGATATCCATGCTATTTATGAAGAACAACAGGGATCGAGA
AACAG

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 9 whose identifier is 3789 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YIL059C and has the DNA sequence

TTTATATGTTAATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCA
GCTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACA
CCGTATATGATAATATACTAGTAACGTAAATACTAGTTAGTAGATGATAG
TTGATTTTTATTCCAACAGTAT

The match between the T1 sequence and the C1/C2 sequence is

TTTATATGTTAATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCA
GCTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACA
CCGTATATGATAATATACTAGTAACGTAAATACTAGTTAGTAGATGATAG
TTGATTTTTATTCCAACA

The match between the T2 sequence and the C1/C2 sequence is

TTTATATGTTAATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCA
GCTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACA
CCGTATATGATAATATACTAGTAACGTAAATACTAGTTAGTAGATGATAG
TTGATTTTTATTCCAACA

A C1/C2 short loop on chromosome 12 whose identifier is 5289 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YLR301W and has the DNA sequence

GGTGAATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATA
TTAGGTATGTAGAATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCAT
AAAAGGGAATCTGCAATTCTACACAATTCTATAAATATTATTATCATCGTT
TTATATGTTAATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAG
CTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACAC
CGTATATGATAATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGT
TGATTTTTATTCCAACAC

The match between the T1 sequence and the C1/C2 sequence is

AGAATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCATAAAAGGGAA
TCTGCAATTCTACACAATTCTATAAATATTATTATCATCGTTTTATATGTTA
ATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAGCTTCCACTAA
TTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACACCGTATATGAT

AATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGTTGATTTTTATT
CCAACA

The match between the T2 sequence and the C1/C2 sequence is

AGGATTTAGGAATCCATAAAAGGGAATCTGCAATTCTACACAATTCTATA
AATATTATTATCATCGTTTTATATGTTAATATTCATTGATCCTATTACATTA
TCAATCCTTGCGTTTCAGCTTCCACTAATTTAGATGACTATTTCTCATCATT
TGCGTCATCTTCTAACACCGTATATGATAATATACTAGTAACGTAAATACT
AGTTAGTAGATGATAGTTGATTTTTATTCCAACA

A C1/C2 short loop on chromosome 13 whose identifier is 5753 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YMR044W and has the DNA sequence

TTGAGAAATGGGGGAATGTTGAGATAATTGTTGGGATTCCATTGTTGATA
AAGGCTATAATATTAGGTATACAGAATATACTAGAAGTTCTCCTCAAGGA
TATAGGAATCCTCAAAATGGAATCTATATTTCTACATACTAATATTACGAT
TATTCCTCATTCCGTTTTATATGTTTCATTATCCTATTACATTATCAATCCT
TGCACTTCAGCTTCCTCTAACTTCGATGACAGCTTCTCATAACTTATGTCA
TCATCTTAACACCGTATATGATAATATATTGATAATATAACTATTAGTTGA
TAGACGATAGTGGATTTTTATTCCAACAT

The match between the T1 sequence and the C1/C2 sequence is

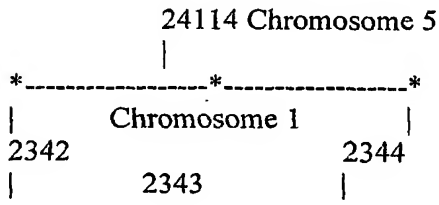
AGATAATTGTTGGGATTCCATTGTTGATAAAGGCTATAATATTAGGTATAC
AGAATATACTAGAAGTTCTCCTC

The match between the T2 sequence and the C1/C2 sequence is

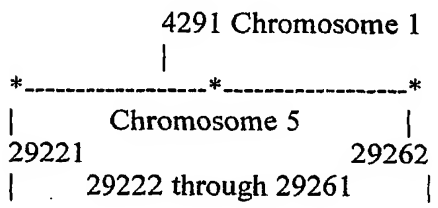
TTGTTGGGATTCCATTGTTGATAAAGGCTATAATATTAGGTATACAGAATA
TACTAGAAGTTCTCCTCAAGGAT

Two examples of multi-celled geneless connectrons – C. elegans

In the first example the existence of the T1-T2 (2342-2344) long loop is controlled by the C1/C2 (24114) short loop. The expression of one C1/C2 (2343) short loop is controlled by the existence of the T1-T2 (2342-2344) long loop.



In the second example the existence of the T1-T2 (29221-29262) long loop is controlled by the C1/C2 (24114) short loop. The expression of one C1/C2 (2343) short loop is controlled by the existence of the T1-T2 (2342-2344) long loop.



A double stranded DNA loop of length 67.059 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 2342. This T1 control element has the DNA sequence

TGAAAACTACAGTAATTCTTTAAATGACTACTGTAGC

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 2344. This T2 control element has the DNA sequence

CTACTGTAGCGCTTGTGTCGATTTACGGGCTCGATTT

There are no genes controlled by this T1/T2 loop.

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 2343 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

TCGACACAAGCGCTACAGTAGCTATTTAAAGAATTACTGTAGTTTTCGCTA CGAGATATTT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 5 whose identifier is 24114 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene C13F10.5 and has the DNA sequence

GCGAAAACTACAGTAATTCTTTAAATGACTACTGTAGCGCTTGTGTCGATT TACGGGCTCGATTTTCG

The match between the T1 sequence and the C1/C2 sequence is

GAAAACTACAGTAATTCTTTAAATGACTACTGTAGC

The match between the T2 sequence and the C1/C2 sequence is

CTACTGTAGCGCTTGTGTCGATTTACGGGCTCGATTT

A double stranded DNA loop of length 41.297 kilo-bases on chromosome 5 is bounded on the left by a T1 sequence whose identifier is 29221. This T1 control element has the DNA sequence

TTTAAATTTCCCGCCAAAAATTGACTGAAAATTTGGATTTTCTTTCCAAAA ATTGACAGAAA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 29262. This T2 control element has the DNA sequence

TGAAAATTTGAATTTCCCGCCAAAAATTAAC

There are no genes controlled by this T1/T2 loop.

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 5 whose identifier is 29222 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

AATTTCCCGCCAAAAATTGACTGAAAATTTGGATTTTCTTTCCAAAAATTG ACAGAAA

This T1-T2 loop also modulates the C1/C2 short loops numbered 29223 to 29260

A C1/C2 short loop on chromosome 5 whose identifier is 29261 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

AAAATTGACTGAAAATTTGAATTTCCAGCCAAAAATTGACTGAAAATTTG
AATT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 1 whose identifier is 4291 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene Y43F8C.5 and has the DNA sequence

AAAATTAACTGAAAATTTGAATTTCCCGCCAAAAATTGACTGAAAATTTG
AATTTCCCGCCAAAAAAAATTGACTGAAAATTTGAATTTCCCGCCAAAAA
TTGACTGAAAATTTGAATTTCCCGCCAAAAATTAATTGAAAATTTGAATTT
CCCGCCAAAAATTAATTGAAACTTTGAATTTTCAA...ATTTCCCGCCAAAA
ATTAATTGAAACTTTGAATTTTCAAATTTCCCGCCAAAAATTGACTGAAAA
TTTGAATTTCCCGCCAAAAATTAATTGAAAATTTGAATTTTTGAATTTCCC
GCCAAAAATGACTGA

The match between the T1 sequence and the C1/C2 sequence is

TTTAAATTTCCCGCCAAAAATTGACTGAAAATTTG

The match between the T2 sequence and the C1/C2 sequence is

AAAAAAATTGACTGAAAATTTGAATTTCCCGCCAAAAATTGA

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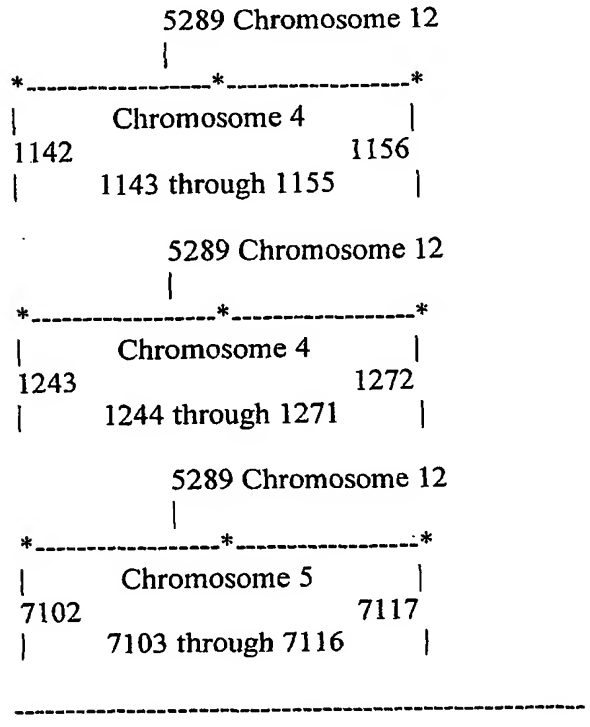
10. One connectron controls many geneless connectrons in single-celled and multi-celled eukaryotes

One C1/C2 short loop can control the existence of many geneless T1-T2 long loops.

Example of a single-celled geneless connectron -- S. cervesiae

In this example the existence of the three T1-T2 (1142-1156, 1242-1272 and 7102-7117) long loops is controlled by the C1/C2 (5289) short loop.



A double stranded DNA loop of length 5.337 kilo-bases on chromosome 4 is bounded on the left by a T1 sequence whose identifier is 1142. This T1 control element has the DNA sequence

ATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATATTAGG
TATGTAGATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCATAAAAG

GGAATCTGCAATTCTACACAATTCTATAAATATTATTATCATCATTTTATA
TGTTAATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAGCTTCC
ACTAATTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACACCGTAT
ATGATAATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGTTGATTT
TTATTCCAACA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1156. This T2 control element has the DNA sequence

TTTTAATAAGGCAATAATATTAGGTATGTAGATATACTAGAAGTTCTCCTC
CAGGATTTAGGAATCCATAAAAGGGAATCTGCAATTCTACACAATTCTAT
AAATATTATTATCATCATTTTATATGTTAATATTCATTGATCCTATTACATT
ATCAATCCTTGCGTTTCAGCTTCCACTAATTTAGATGACTATTTCTCATCAT
TTGCGTCATCTTCTAACACCGTATATGATAATATACTAGTAACGTAAATAC
TAGTTAGTAGATGATAGTTGATTTTTATTCCAACAAGAA

There are no genes controlled by this T1/T2 loop.

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 4 whose identifier is 1143 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

ATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATATTAGG
TATGTAGATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCATAAAAG
GGAATCTGCAATTCTACACAATTCTATAAATATTATTATCATCATTTTATA
TGTTAATATTCATTGATCCTATTACATTATCAAT...CTCTAAGTCTCATTGCC
TTTGTGCCAAAAAATCTGTTTCTAAATTTCTCTTCATTTGTAGACTTAATTA
TACTGATCGTTGATCTACTATCAGTAAGTAAGCCTTTAATAATTGGTTTCT
TGTTAAGTTCTTGCACAAGGTGACTGAGGTTATTCAATAGCGG

This T1-T2 loop also modulates the C1/C2 short loops numbered 1144 to 1154

A C1/C2 short loop on chromosome 4 whose identifier is 1155 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

GAGGAGAACTTCTAGTATATCTACATACCTAATATTATTGCCTTATTAAAA
ATGGAATCCCAACAATTA

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 12 whose identifier is 5289 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YLR301W and has the DNA sequence

GGTGAATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATA
TTAGGTATGTAGAATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCAT
AAAAGGGAATCTGCAATTCTACACAATTCTATAAATATTATTATCATCGTT
TTATATGTTAATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAG
CTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACAC
CGTATATGATAATATACTAGTACGTAAATACTAGTTAGTAGATGATAGTT
GATTTTTATTCCAACAC

The match between the T1 sequence and the C1/C2 sequence is

ATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATATTAGG
TATGTAGA

The match between the T2 sequence and the C1/C2 sequence is

TTTTAATAAGGCAATAATATTAGGTATGTAGA

A double stranded DNA loop of length 5.251 kilo-bases on chromosome 4 is bounded on the left by a T1 sequence whose identifier is 1243. This T1 control element has the DNA sequence

CGTGTTTTATCTCATGTTGTTCGTTTTGTTATTGAGATATATGTGGGTAATT
AGATAATTGTTGGGATTCCATTGTTGATAAAGGCTATAATATTAGGTATAC
AGAATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCATAAAAGGGAA
TCTGCAATTCTACACAATTCTATAAATATTATTATCATCGTTTTATATGTTA
ATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAGCTTCCACTAA
TTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACACCGTATATGAT
AATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGTTGATTTTTATT
CCAACA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 1272. This T2 control element has the DNA sequence

TGAGATATATGTGGGTAATTAGATAATTGTTGGGATTCCATTGTTGATAAA
GGCTATAATATTAGGTATACAGAATATACTAGAAGTTCTCCTCGAGGATTT
AGGAATCCATAAAAGGGAATCTGCAATTCTACACAATTCTATAAATATTA
TTATCATCGTTTTATATGTTAATATTCATTGATC...TATACTAGTAACGTAA
ATACTAGTTAGTAGATGATAGTTGATTTTTATTCCAACAGTTATAAGGTTG
TTTCATATGTGTTTTATGAA

There are no genes controlled by this T1/T2 loop.

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 4 whose identifier is 1244 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

TTTATCTCATGTTGTTCGTTTTGTTATTGAGATATATGTGGGTAATTAGATA
ATTGTTGGGATTCCATTGTTGATAAAGGCTATAATATTAGGTATACAGAAT
ATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCATAAAAGGGAATCTGC
AATTCTACACAATTCTATAAATATTATTATCAT...GTCTCGATGTAGTATAC
GTATAAATTATTACCTGATACTTCATCTCTAAGTCTCATTGCCTTTGTGCCA
AAAAATCTGTTTCTAAATTTCTCTTCATTTGTAGACTTAATTATACTGATCG
TTGATCTACTATCAGTAAGT

This T1-T2 loop also modulates the C1/C2 short loops numbered 1245 to 1270

A C1/C2 short loop on chromosome 4 whose identifier is 1271 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

TGTTGTATCTCAAAATGAGATATGTCAGTATGACAATACGTCATCCTAAAC
GTTCATAAAACACATATGAAACAACCTTATAACTGTTGGAATAAAAATCA
ACTATCATCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGG
TGTTAGAAGATGACGCAAATGATGAGAAATAGTC...CAACAATGGAATCC
CAACAATTATCTAATTACCCACATATATCTCATGGTAGCGCCTGTGCTTCG
GTTACTTCTAAGGAAGTCCACACAAATCAAGATCCGTTAGACGTTTCAGC
TTCCAAAA

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 12 whose identifier is 5289 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed

as a RNA single strand that is 3'UTR to the gene YLR301W and has the DNA sequence

GGTGAATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATA
TTAGGTATGTAGAATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCAT
AAAAGGGAATCTGCAATTCTACACAATTCTATAAATATTATTATCATCGTT
TTATATGTTAATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAG
CTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACAC
CGTATATGATAATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGT
TGATTTTTATTCCAACAC

The match between the T1 sequence and the C1/C2 sequence is

AGAATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCATAAAAGGGAA
TCTGCAATTCTACACAATTCTATAAATATTATTATCATCGTTTTATATGTTA
ATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAGCTTCCACTAA
TTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACACCGTATATGAT
AATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGTTGATTTTTATT
CCAACA

The match between the T2 sequence and the C1/C2 sequence is

AGAATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCATAAAAGGGAA
TCTGCAATTCTACACAATTCTATAAATATTATTATCATCGTTTTATATGTTA
ATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAGCTTCCACTAA
TTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACACCGTATATGAT
AATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGTTGATTTTTATT
CCAACA

A double stranded DNA loop of length 5.296 kilo-bases on chromosome 15 is bounded on the left
by a T1 sequence whose identifier is 7102. This T1 control element has the DNA sequence

CATGATTAATATGACCAATCGGCGTGTGTTTTTGAAAAGTGGGTGAATTTT
GAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATATTAGGTATGT
AGAATGTACTAGAAGTTCTCCTCAAGGATTTAGGAATCCATGAAAGGGAA
TCTGCAATTCTACACAATTCTATAAATATTATTATCATCATTTTATATGTTA
ATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAGCTTCCACTAA
TTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACACCGTATATGAT
AATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGTTGATTTTTATT
CCAACA

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 7117. This T2 control element has the DNA sequence

TGAAAAGTGGGTGAATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAG
GCAATAATATTAGGTATGTAGAATGTACTAGAAGTTCTCCTCAAGGATTT
AGGAATCCATGAAAGGGAATCTGCAATTCTACACAATTCTATAAATATTA
TTATCATCATTTTATATGTTAATATTCATTGATCCTATTACATTATCAATCC
TTGCGTTTCAGCTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGTCA
TCTTCTAACACCGTATATGATAATATACTAGTAACGTAAATACTAGTTAGT
AGATGATAGTTGATTTTTATTCCAACAGTTTTATATACCTCTCTTATTTAGT
ATAAGAA

There are no genes controlled by this T1/T2 loop.

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 15 whose identifier is 7103 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

AAGAACATTGCTGATGTGATGACAAAACCTCTTCCGATAAAAACATTTAA
ACTATTAACTAACAAATGGATTCATTAGATCTATTACATTATGGGTGGTAT
GTTGGAATAAAAATCAACTATCATCTACTAACTAGTATTTACGTTACTAGT
ATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAGAAATAGTC
ATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTAATAGGATC
AATGAATATTAACATATAAAATGATGATAATAATATTTATAGAATTGTGT
AGAATTGCAGATTCCCTTTCATGGATTCCTAAATCCTTGAGGAGAACTTCT
AGTA

This T1-T2 loop also modulates the C1/C2 short loops numbered 7104 to 7115

A C1/C2 short loop on chromosome 15 whose identifier is 7116 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

CCATTCTGTGGAGGTGGTACTGAAGCAGGTTGAGGAGAGACATGATGATG
GTTCTCTGGAACAGCT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 12 whose identifier is 5289 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene YLR301W and has the DNA sequence

GGTGAATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATA
TTAGGTATGTAGAATATACTAGAAGTTCTCCTCGAGGATTTAGGAATCCAT

AAAAGGGAATCTGCAATTCTACACAATTCTATAAATATTATTATCATCGTT
TTATATGTTAATATTCATTGATCCTATTACATTATCAATCCTTGCGTTTCAG
CTTCCACTAATTTAGATGACTATTTCTCATCATTTGCGTCATCTTCTAACAC
CGTATATGATAATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGT
TGATTTTTATTCCAACAC

The match between the T1 sequence and the C1/C2 sequence is

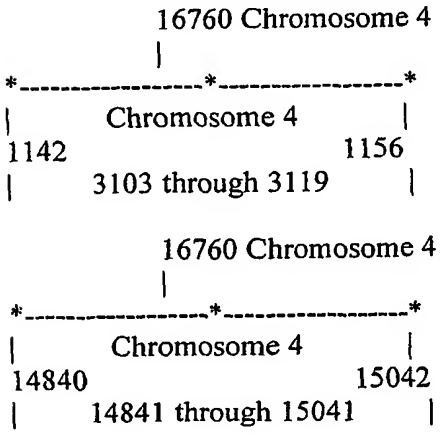
GGTGAATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATA
TTAGGTATGTAGAAT

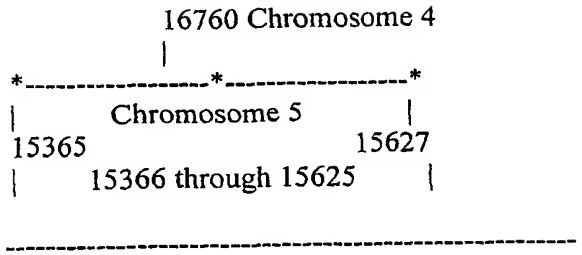
The match between the T2 sequence and the C1/C2 sequence is

GGTGAATTTTGAGATAATTGTTGGGATTCCATTTTTAATAAGGCAATAATA
TTAGGTATGTAGAAT

Example of a multi-celled geneless connectron – C. elegans

In this example the existence of the three T1-T2 (1142-1156, 14840-15042 and 15365-15627) long loops is controlled by the C1/C2 (16760) short loop.





A double stranded DNA loop of length 15.894 kilo-bases on chromosome 1 is bounded on the left by a T1 sequence whose identifier is 3101. This T1 control element has the DNA sequence

CAAATCGGCAAATTGCCGGAATTGAACATTTCC

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 3120. This T2 control element has the DNA sequence

AAACGATTTTTCCGGCAAATCGGCAAATTGCCGGAATTGTAATTTCCGGC AAAT

There are no genes controlled by this T1/T2 loop.

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 1 whose identifier is 3103 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

TTAAAATTTCCGGCAAATCGGCAAATTGGCAGAAATGAAACTCACGGCAA ATCGG

This T1-T2 loop also modulates the C1/C2 short loops numbered 3104 to 3118

A C1/C2 short loop on chromosome 1 whose identifier is 3119 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

CCCGCATTTTTTGTAGATCAAACCGTAATGGGACGGCCTGGCAACACGTG
ATTTTCCAAAT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 4 whose identifier is 16760 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene T23E1.2 and has the DNA sequence

GGCAAATTGCCGAAATTGAACATTTCCGGCAAATCGGCAAATTGCCGGAA
TTGAACATTTCCGGCAAATCGGCAAATTGCCGGAATTGAACATTTCCGGC
AAATCGGCAAATTGCCGGAATTGA

The match between the T1 sequence and the C1/C2 sequence is

CAAATCGGCAAATTGCCGGAATTGAACATTTCC

The match between the T2 sequence and the C1/C2 sequence is

TTTCCGGCAAATCGGCAAATTGCCGGAATTG

A double stranded DNA loop of length 86.977 kilo-bases on chromosome 3 is bounded on the left by a T1 sequence whose identifier is 14840. This T1 control element has the DNA sequence

AAAAATTTCCGGCAAGTCGGCAATTTTCCGAAAATGAAAATTTCCGGCAA
ATCGGCAAATTGCCGGAATTGAAAATTCCTGGCAAATCAGCAAATTTGCG
GCAAATCGGCAATTTGCCGAAAATGAAAATTTCCGGCAAAT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 15042. This T2 control element has the DNA sequence

CAAATCGGTAGGTAAATTGGCCAAACTTGAAAATTTCCGGCAAATCGGCA
AATTCCGCGAACTGAACATTTCCGGCAAATCGGCAAATTGCTCGAACT

There are no genes controlled by this T1/T2 loop.

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 3 whose identifier is 14841 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

AAAAATTTCCGGCAAGTCGGCAATTTTCCGAAAATGAAAATTTCCGGCAA
ATCGGCAAATTGCCGGAATTGAAAATTCCTGGCAAATCAGCAAATTTGCG
GCAAATCGGCAATTTGCCGAAAATGAAAATTTCCGGCAAAT

This T1-T2 loop also modulates the C1/C2 short loops numbered 14842 to 15040

A C1/C2 short loop on chromosome 3 whose identifier is 15041 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

CGGCAATTGCCGTTCGGCAATTTGCCAATTTGCCGGAAATTTTCAATTCCG
GCAA

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 4 whose identifier is 16760 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene T23E1.2 and has the DNA sequence

GGCAAATTGCCGAAATTGAACATTTCCGGCAAATCGGCAAATTGCCGGAA
TTGAACATTTCCGGCAAATCGGCAAATTGCCGGAATTGAACATTTCCGGC
AAATCGGCAAATTGCCGGAATTGA

The match between the T1 sequence and the C1/C2 sequence is

ATTTCCGGCAAATCGGCAAATTGCCGGAATTGAA

The match between the T2 sequence and the C1/C2 sequence is

TGAACATTTCCGGCAAATCGGCAAATTGC

A double stranded DNA loop of length 98.488 kilo-bases on chromosome 3 is bounded on the left by a T1 sequence whose identifier is 15365. This T1 control element has the DNA sequence

AAAATTTCCGGCAAATCGGCAATTTGCCAAAAATTGAAATTTCCGGCAAA
TCGGCAATTTGTCAAAAATGAAAATTTCCGGCAAATCGGCAAATTGCCGA
AAATGAAAATTTCCGGCAAATCGGCAAACTTCCGGAACTGAAAATTTCCG
GCAAATCGGCAATTTGCCATAAATGAACATTTCCGG...GGCGAAAATTAAA
ATTTCCGCCATATCGGCAATTTGCCAAAAAATTAAAATTTCCGGCAAATC

GGCAAATTGCCGGAATTCAAAATTTCCGGCAAACCGGCAAATTGCCGGAA CTCAAAATTCCCGGCAAATCAGCAAATTGCCGGAATT

This double stranded DNA loop is bounded on the right by a T2 control element whose identifier is 15627. This T2 control element has the DNA sequence

TGGCAAACCGGCAAATTGCCGGAATTGAACATTTCCGGCAAATCGGCAAT TTGCCGGAATTGAAATTT

There are no genes controlled by this T1/T2 loop.

This long T1/T2 double stranded DNA loop modulates the expression of the following C1/C2 short loops

A C1/C2 short loop on chromosome 3 whose identifier is 15366 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

TGCCGATTTGCCGGAAATTTTCATTTTCGGCAATTTGCCGATTTGCCGGAA ATTTTCATT

This T1-T2 loop also modulates the C1/C2 short loops numbered 15366 to 15624

A C1/C2 short loop on chromosome 3 whose identifier is 15625 controls the expression of the genes of one or more other T1/T2 long loops. This C1/C2 short loop has the DNA sequence

TCAAGCAAATTGTCAAATTCGCGGAACTAAACATTTCCGGCAAATCGGCA AATT

The expression of genes in this T1/T2 long loop is controlled by the following C1/C2 short loops.

A C1/C2 short loop on chromosome 4 whose identifier is 16760 controls the expression of the genes in this T1/T2 long loop. This C1/C2 short loop is expressed as a RNA single strand that is 3'UTR to the gene T23E1.2 and has the DNA sequence

GGCAAATTGCCGAAATTGAACATTTCCGGCAAATCGGCAAATTGCCGGAA
TTGAACATTTCCGGCAAATCGGCAAATTGCCGGAATTGAACATTTCCGGC
AAATCGGCAAATTGCCGGAATTGA

The match between the T1 sequence and the C1/C2 sequence is

ATTTCCGGCAAATCGGCAAATTGCCGGAATT

The match between the T2 sequence and the C1/C2 sequence is

CGGCAAATTGCCGGAATTGAACATTTCCGGCAAATCGGCAA

Claims

What is claimed is:

1. A method of identifying DNA sequences that control the expression of different collections of genes in a genome comprising, detecting selected DNA sequences adjacent to some genes excluding exons and introns.

2. A method of identifying DNA sequences that control the expression of different collections of genes comprising, detecting, by computer, one or more pairs of non-adjacent DNA sequences to which are bound to two RNA sequences.

3. A method of identifying DNA sequences that control the expression of different collections of genes in a genome comprising detecting changes in connectron behavior in the genome.

4. A method of modifying the expression of different gene collections in a genome, comprising detecting changes in connectron behavior as a result of an exogenous stimulus.

5. A method of detecting where and when new genes are being integrated into a host genome comprising detecting the connectrons in said host genome.

6. A method of detecting the expression effect of different gene collections in a given body comprising detecting the back and forth flow of connectrons between the chromosomes thereof.

7. A method of modifying a given body comprising modifying the connectron organization therein.

8. A method of detecting connectron control and target sequences in a given genome comprising:

determining the base composition of said genome,
determining one or more sites of control sequence organization, and/or
determining one or more sites of target application.

9. A method of determining the response of a cell in any tissue to changes in the cell's environment and/or genetic composition comprising providing a complete genomic DNA sequence for the organism and determining the effect of changes in connectrons due to application of a given exogenous stimulus to the gnome.

10. In prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the tetradic relationship T1=C1 and T2=C2 where T1 and T2 are DNA sequences 20 or more bases in length, where the C1 sequence is adjacent to the C2 sequence, where the T1 and T2 sequences are on the same chromosome, and where the C1/C2 sequences are on the same chromosome as T1 and T2 or where the C1/C2 sequences are on a chromosome different from T1 and T2, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

11. In prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits many different C1/C2 short loops to control the existence of a T1-T2 long loop and wherein said C1/C2 short lops can be on the same chromosome or on different chromosomes from the T1-T2 long loop, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 540 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

12. In prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of many T1-T2 long loops, the C1/C2 short loop can be on the same chromosome or on different chromosomes from the T1-T2 long loops, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

13. The connectron relationships between prokaryotes and their plasmids wherein said connectrons implement a control mechanism between the two genomes that makes it possible from them to form a symbiotic relationship, and in the case of D. radiodurans the relationship is not symmetric, and the D. radiodurans genome sends C1/C2 short loops to the MP1 plasmid, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

14. The connectron relationships that exist in plant and higher animals.

15. In prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of one or more T1-T2 long loops without being subject to any expression controls other than those of the gene to which the C1/C2 is 3'UTR, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart,

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart, and

3'UTR - untranslated 3' end of an mRNA is beyond the end of the last exon, a stop codon in the mRNA causes the ribosome to stop the translation of mRNA into protein.

16. In prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of one or more T1-T2 long loops such that this C1/C2 short loop is itself subject to expression control by another T1-T2 long loop which surrounds it, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

17. In prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of the T1-T2 long loop that surrounds it, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 50 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

18. The connectron relationship that do not have any genes within the T1-T2 long loop, wherein:

T1 sequence is any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, and the T2 or T1 sequences must be between about 1kb and 105kb apart.

19. The geneless connectron relationship where one C1/C2 short loop controls the existence of many geneless T1-T2 long loops, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

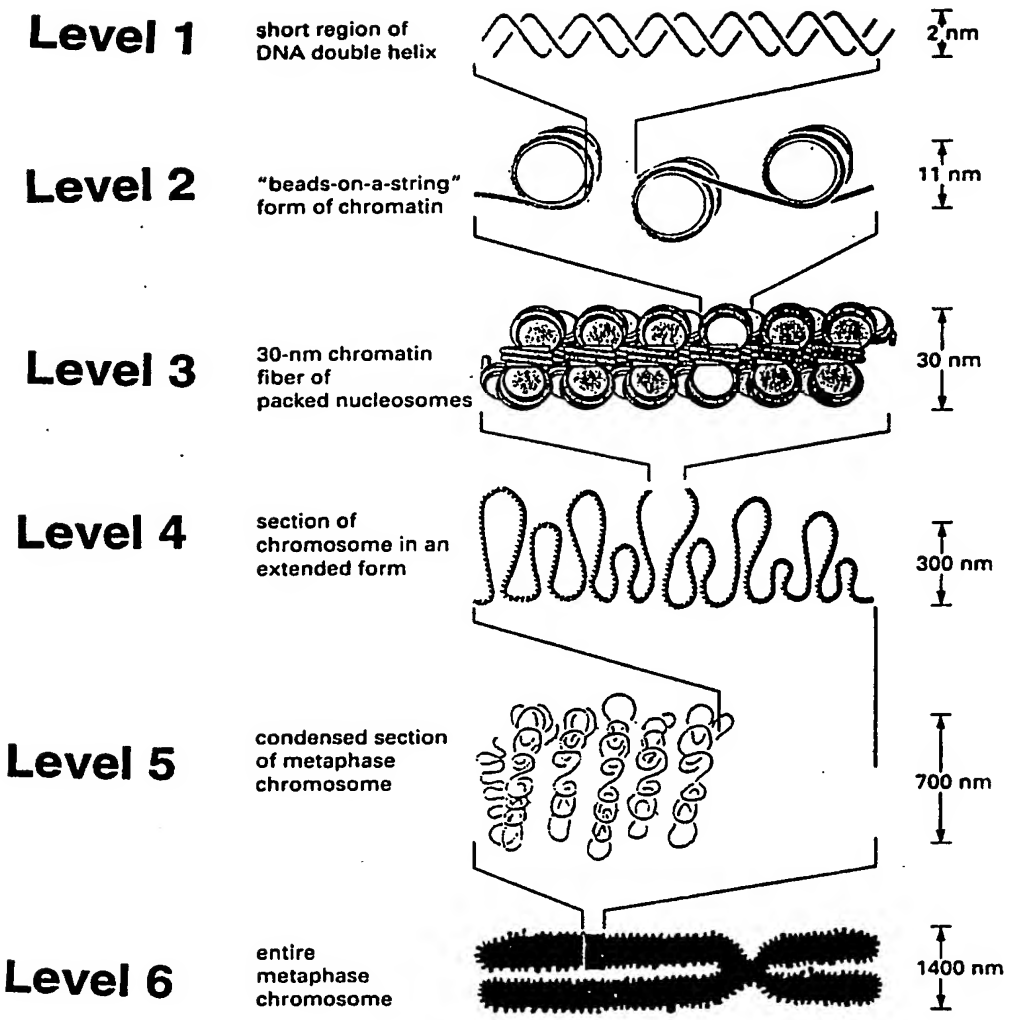
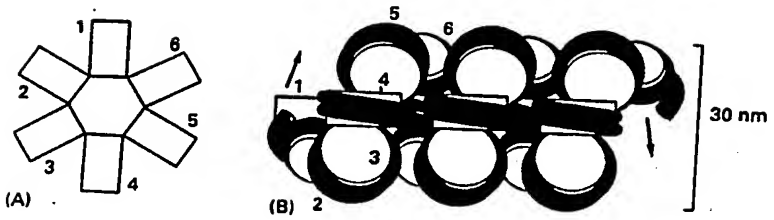
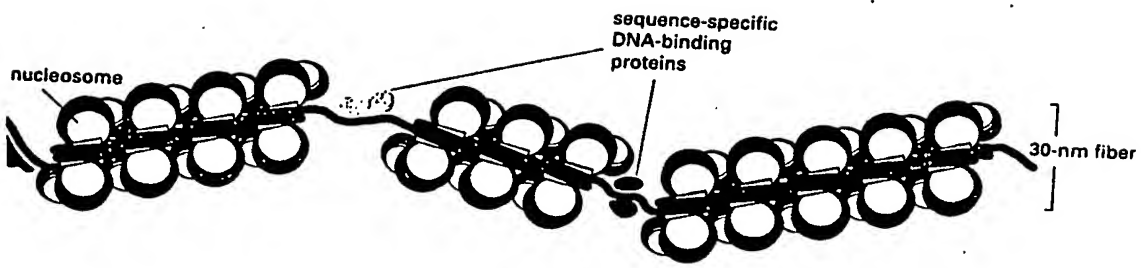

Level 1
short region of DNA double helix
2 nm
Level 2
"beads-on-a-string" form of chromatin
11 nm
Level 3
30-nm chromatin fiber of packed nucleosomes
30 nm
Level 4
section of chromosome in an extended form
300 nm
Level 5
condensed section of metaphase chromosome
700 nm
Level 6
entire metaphase chromosome
1400 nm

Figure 1


1
6
2
5
3
4
(A)
5
6
1
4
3
(B) 2
30 nm

(a)


nucleosome
sequence-specific
DNA-binding
proteins
30-nm fiber

(b)

Figure 2

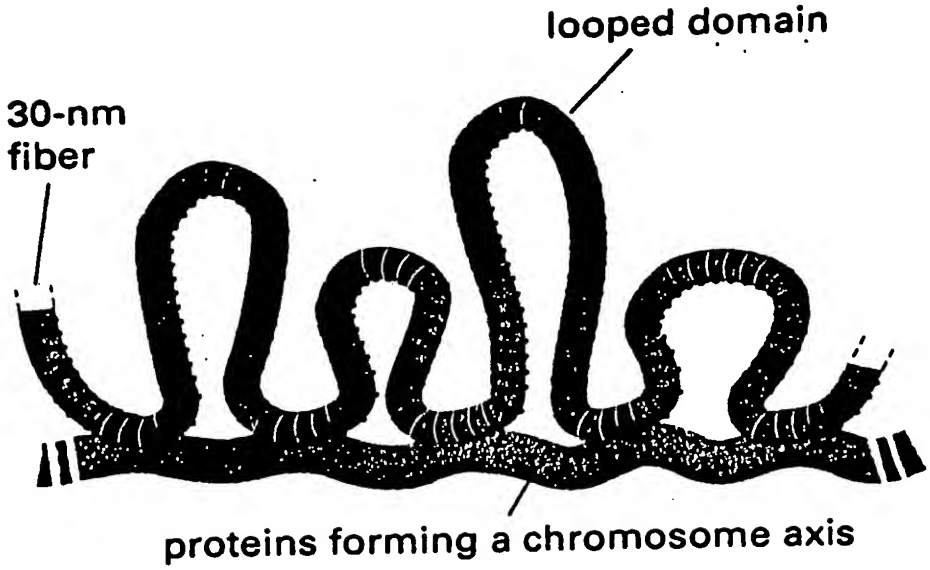

looped domain
30-nm
fiber
proteins forming a chromosome axis

Figure 3

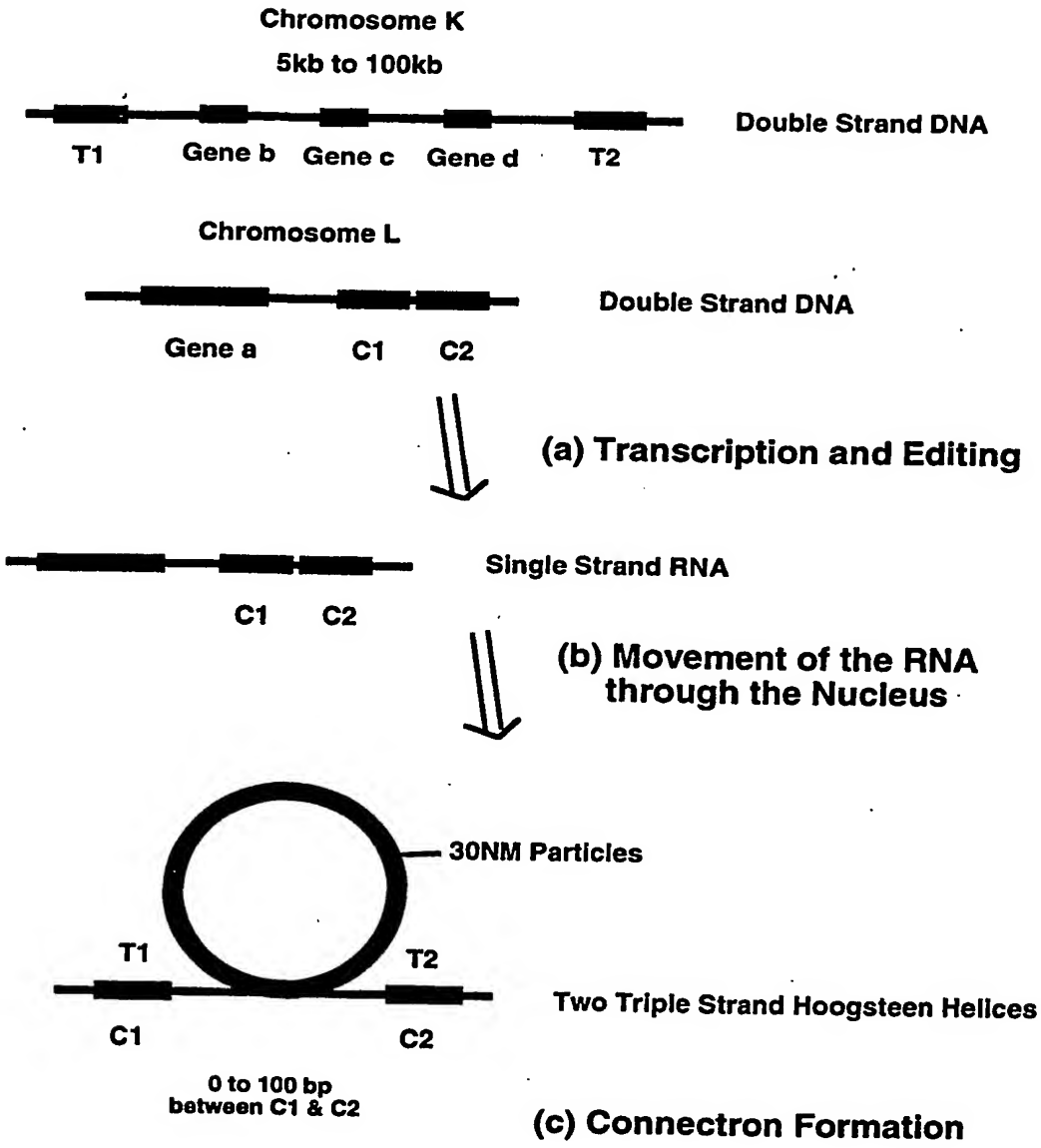

Chromosome K
5kb to 100kb
Double Strand DNA
T1
Gene b
Gene c
Gene d
T2
Chromosome L
Double Strand DNA
Gene a
C1
C2
(a) Transcription and Editing
Single Strand RNA
C1
C2
(b) Movement of the RNA through the Nucleus
30NM Particles
T1
T2
Two Triple Strand Hoogsteen Helices
C1
C2
0 to 100 bp between C1 & C2
(c) Connectron Formation

Figure 4

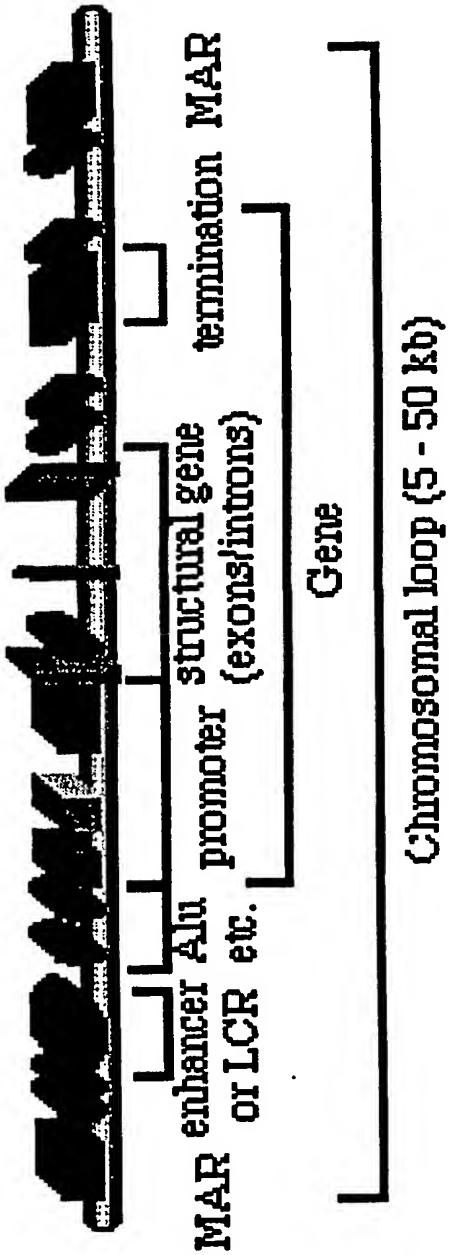


Figure 5

Genome	Chromosome Number	Number of Genes	Chromosome Length (bp)	Total Number of C1/C2 Short Loops	Total Number of T1/T2 Long Loops	Number of Unique C1/C2 Short Loops	Number of Unique T1/T2 Long Loops	Percent of Genes Controlled
				Table 1				
E. coli	I	4,289	4,639,221	544	544	214	178	24.78
H. pylori	I	1,566	1,667,867	19	19	17	10	10.53
M. jannaschii	I	1,715	1,664,970	1,648	1,648	122	360	35.12
D. radiodurans	I	2,580	2,648,638	974	628	246	292	
	II	357	412,348	113	14	17	10	
	III - Plasmid MP1	131	177,466	803	1,259	87	464	
	IV - Plasmid CP1	35	45,704	91	80	28	45	77.14
	Totals	3,103	3,284,156	1,981	1,981	378	811	
S. cerveslae	I	110	230,209	898	283	26	112	
	II	447	813,137	1,387	2,516	568	1,094	
	III	172	315,339	1,314	1,762	336	553	
	IV	845	1,520,519	4,253	3,689	1,298	1,279	
	V	280	576,870	2,034	2,888	638	1,111	
	VI	127	270,148	438	155	153	45	
	VII	629	1,090,936	3,003	2,776	981	982	
	VIII	279	562,638	1,207	410	433	166	
	IX	236	439,885	248	81	113	48	
	X	406	745,440	1,691	2,019	541	768	
	XI	351	666,448	513	228	128	68	
	XII	578	1,078,173	3,010	4,282	951	1,921	
	XIII	501	924,430	2,305	3,254	680	1,229	
	XIV	458	784,328	1,579	490	528	144	
	XV	609	1,091,283	1,630	626	543	210	
	XVI	510	948,066	2,628	2,680	820	967	
	Totals	6,538	12,057,849	28,139	28,139	8,737	10,697	19.88
C. elegans	I	2,474	16,183,833	315,926	159,815	12,245	24,537	
	II	3,043	17,004,925	133,735	92,585	13,370	26,647	
	III	2,100	12,114,540	93,171	897,303	8,472	138,469	
	IV	2,523	15,887,371	67,196	99,562	10,641	14,420	
	V	4,358	21,280,512	337,841	246,674	15,612	33,571	
	X	2,625	17,624,844	611,789	63,719	6,138	7,805	
	Totals	17,123	100,096,025	1,559,658	1,559,658	66,478	245,449	33.6

Table 1 - page 1

Genome	Chromosome Number	Number of Genes	Chromosome Length (bp)	Total Number of C1/C2 Short Loops	Total Number of T1/T2 Long Loops	Number of Unique C1/C2 Short Loops	Number of Unique T1/T2 Long Loops	Percent of Genes Controlled
	Scaffold							
D. megalomaster	1	1,138	10,564,115	16,200	17,916	3,268	5,015	
	2	698	4,515,887	3,283	9,317	955	2,634	
	3	633	5,077,262	3,502	3,027	1,038	556	
	4	1,075	9,080,116	129,140	127,538	1,566	5,910	
	5	1,777	15,101,630	16,800	16,463	2,565	2,093	
	6	122	1,265,848	668	237	190	110	
	7	28	536,527	476	586	208	378	
	8	615	4,861,285	10,727	10,731	603	978	
	9	317	2,692,893	2,506	759	624	214	
	10	286	2,159,491	1,436	1,049	494	369	
	11	1,822	16,346,801	8,583	8,415	2,363	1,860	
	12	143	1,363,555	151	15	64	13	
	13	3,075	24,259,494	11,273	9,274	3,133	1,608	
	14	49	705,960	1,922	1,754	606	662	
	15	91	1,361,891	3,544	4,719	907	2,721	
	16	66	509,295	101	106	42	28	
	17	1,893	13,672,780	6,770	3,286	1,929	739	
	18	61	751,204	1,451	2,521	490	1,596	
	19	35	403,964	471	1,291	212	926	
	Totals	13,924	115,228,998	219,014	219,014	21,257	28,411	5.21
A. thaliania	Ia	3,221	14,221,815	22,735	20,165	3,310	4,603	
	Ib	3,136	14,668,883	22,202	25,016	4,043	7,324	
	II	4,036	19,647,091	153,605	75,591	10,377	19,290	
	IV	3,823	17,550,082	523,824	601,594	6,445	54,956	
	Totals	14,216	66,087,871	722,366	722,366	24,175	86,173	7.51
H. sapiens	XXI	position data	33,667,731		> 10,000			
		not available						

Table 1 - page 2

Chromosome of T1-T2

Chromosome of C1/C2	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	**39**	57	35	57	4	5	19	2		41		38	25	7	12	12
2	9	**70**	13	27	98		22	17	1		9	36	130	15		89
3	6		**54**	44	39		37	5	1		5	16	23	10	6	29
4	10	73	93	**257**	158	13	138	12	2	67	9	135	144	30	38	125
5	1	47	13	42	**32**	5	19		1	26		76	14	5	9	18
6												46				
7	4	72	46	114	83	7	**100**	14	2	64	6	83	91	15	20	73
8	10	66	13	52			25	**14**	3	25		58	15	3	12	16
9	2			12	14		18	9	**2**	1		4		2	4	8
10	4	9	24	48	107	1	47	9	1	**59**	8	38	100	10	8	81
11		27	15	39	1		15			26	**5**	6	29	1	11	14
12	10	68	61	107	90	8	77	2		56	2	**193**	73	19	25	76
13	4	78	60	134	85	2	68	8	3	71	14	60	**173**	10	28	127
14		66	13	56	14		16			25		15	18	**4**	12	28
15	3	10	20	31	79	1	27	11	1	8	8	52	78	6	7	82
16	6	54	68	126	121	9	86	14	1	51	15	100	130	20	24	**137**

Table 2

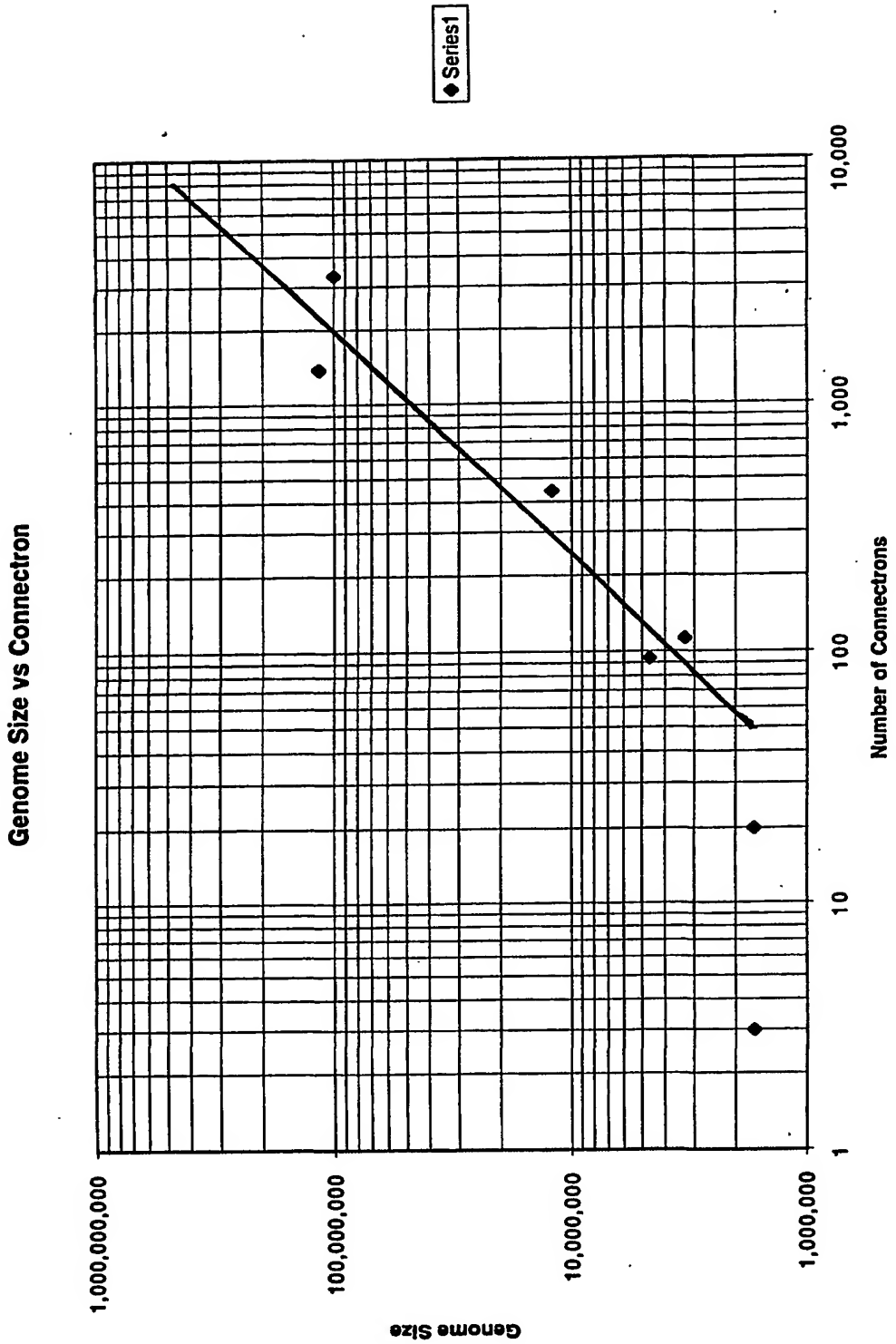

Series1
Genome Size vs Connectron
Genome Size
1,000,000,000
100,000,000
10,000,000
1,000,000
Number of Connectrons
10,000
1,000
100
10
1

Figure 6

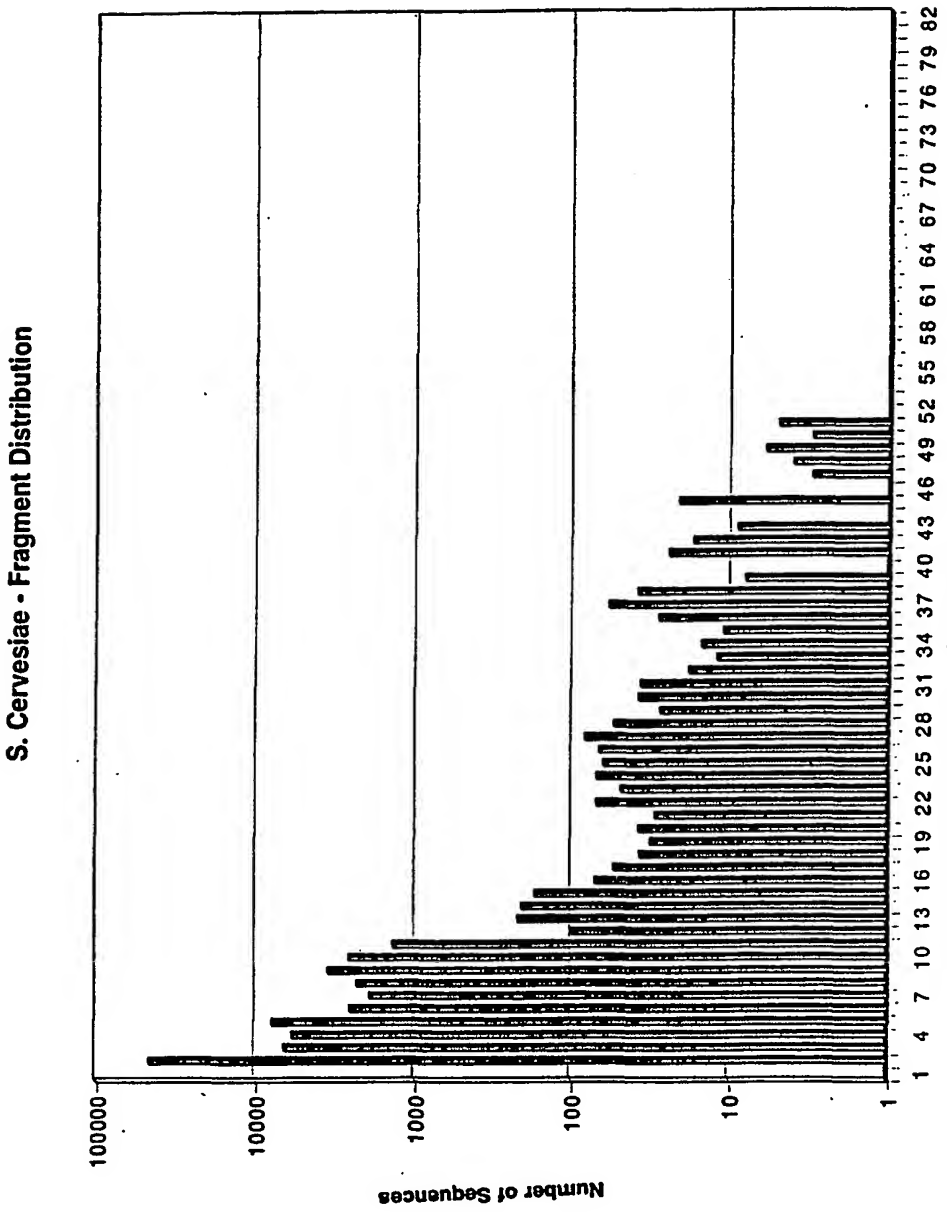


Figure 7

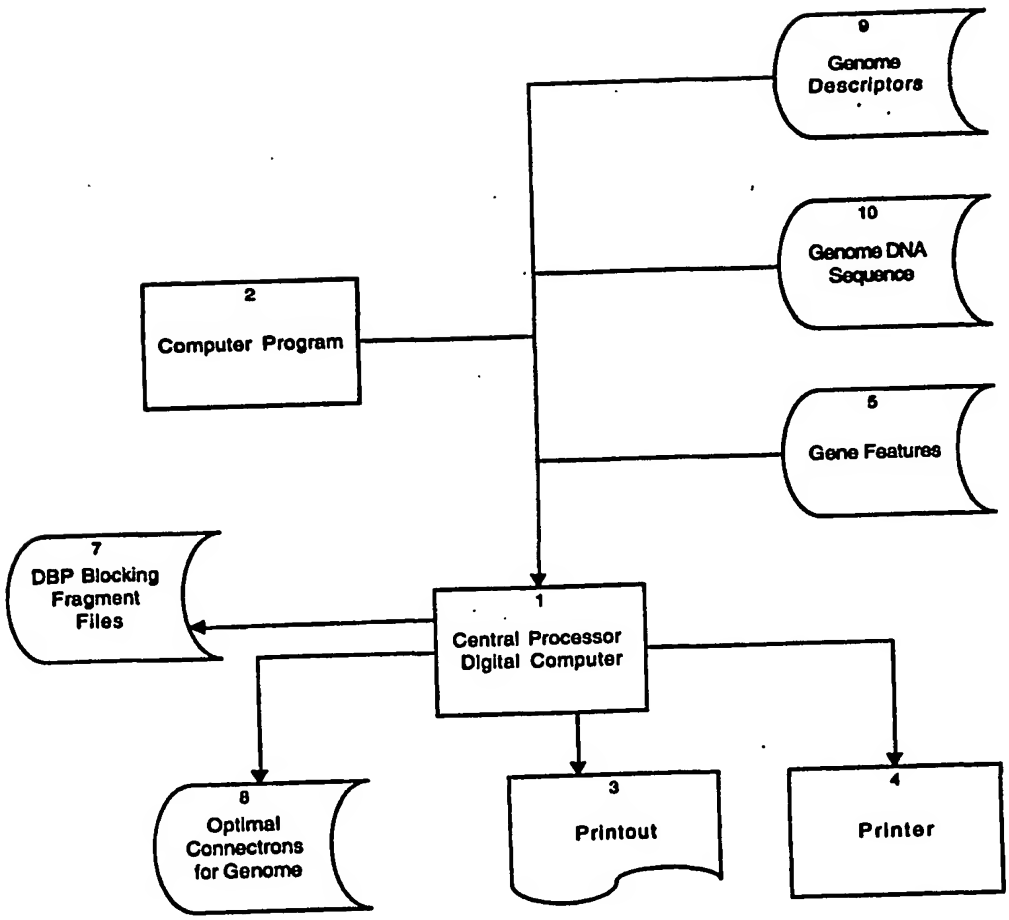


Figure 8

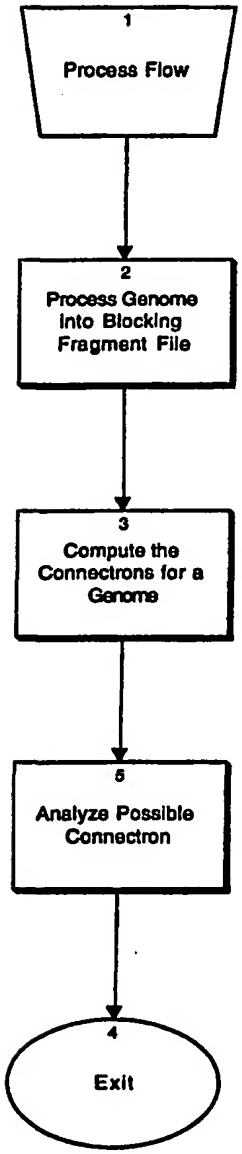

1
Process Flow
2
Process Genome into Blocking Fragment File
3
Compute the Connectrons for a Genome
5
Analyze Possible Connectron
4
Exit

Figure 9

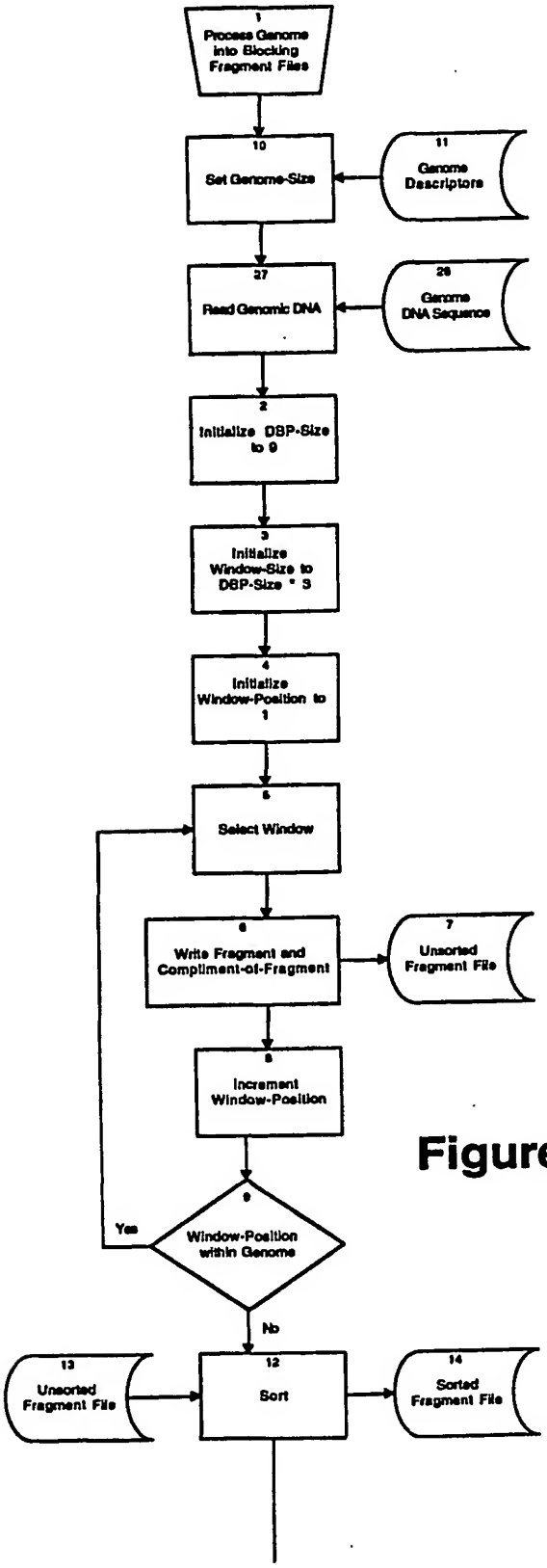


Figure 10 - page 1

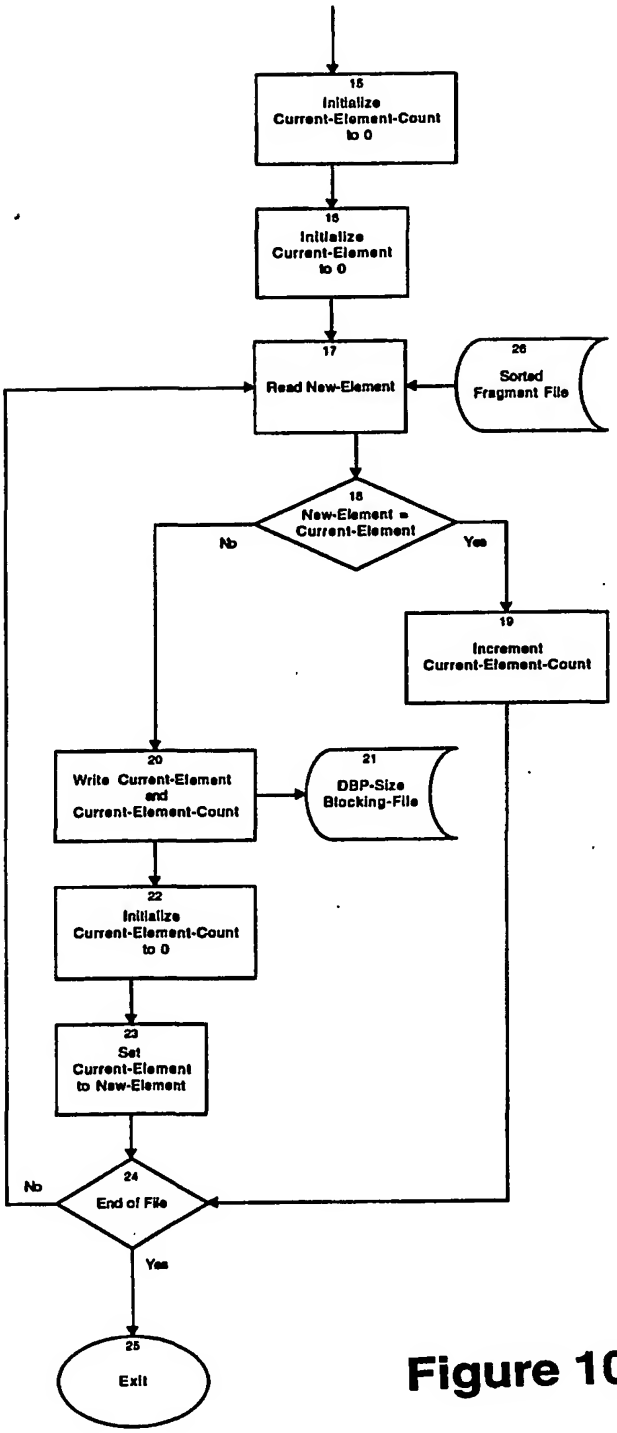
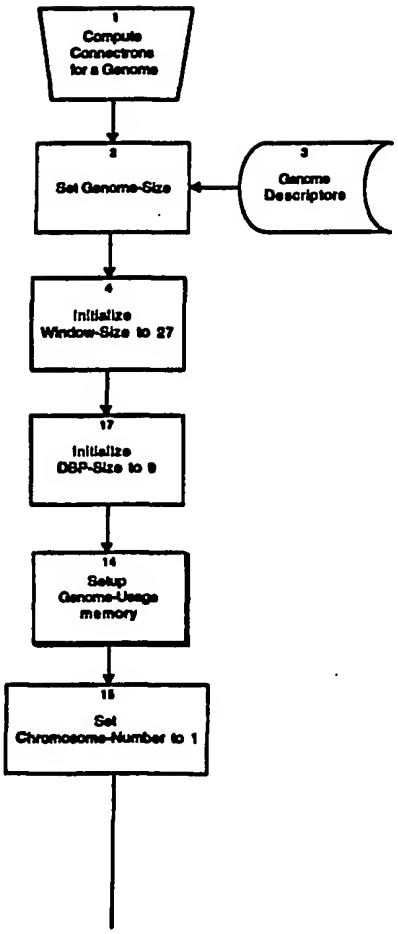


Figure 10 - page 2

Figure 11 - page 1



see Figure 13

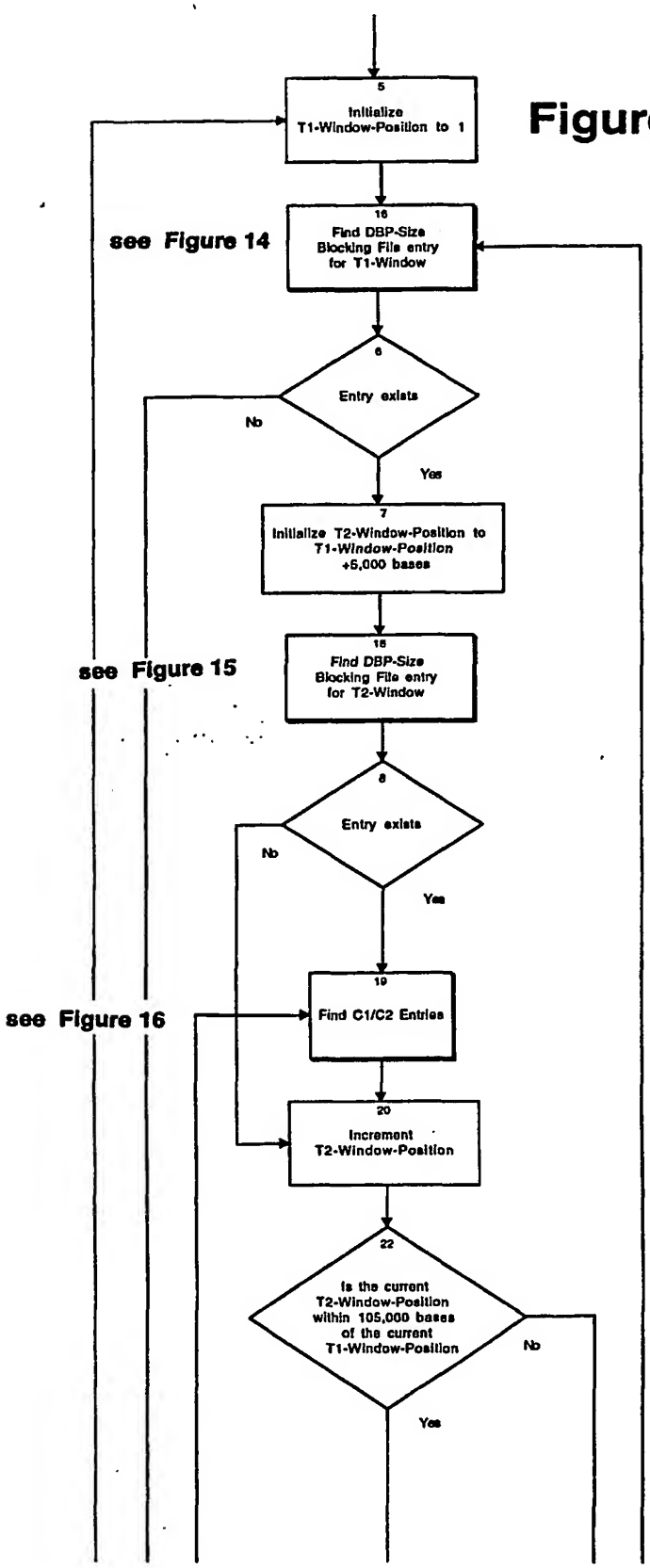


Figure 11 - page 2

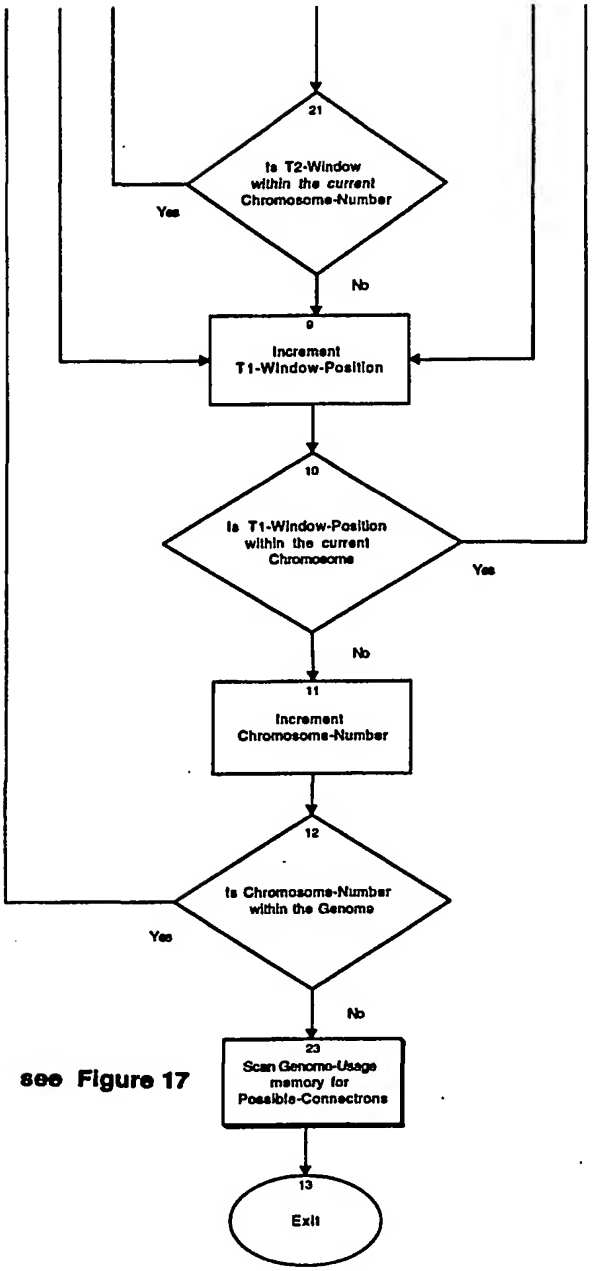


Figure 11 - page 3

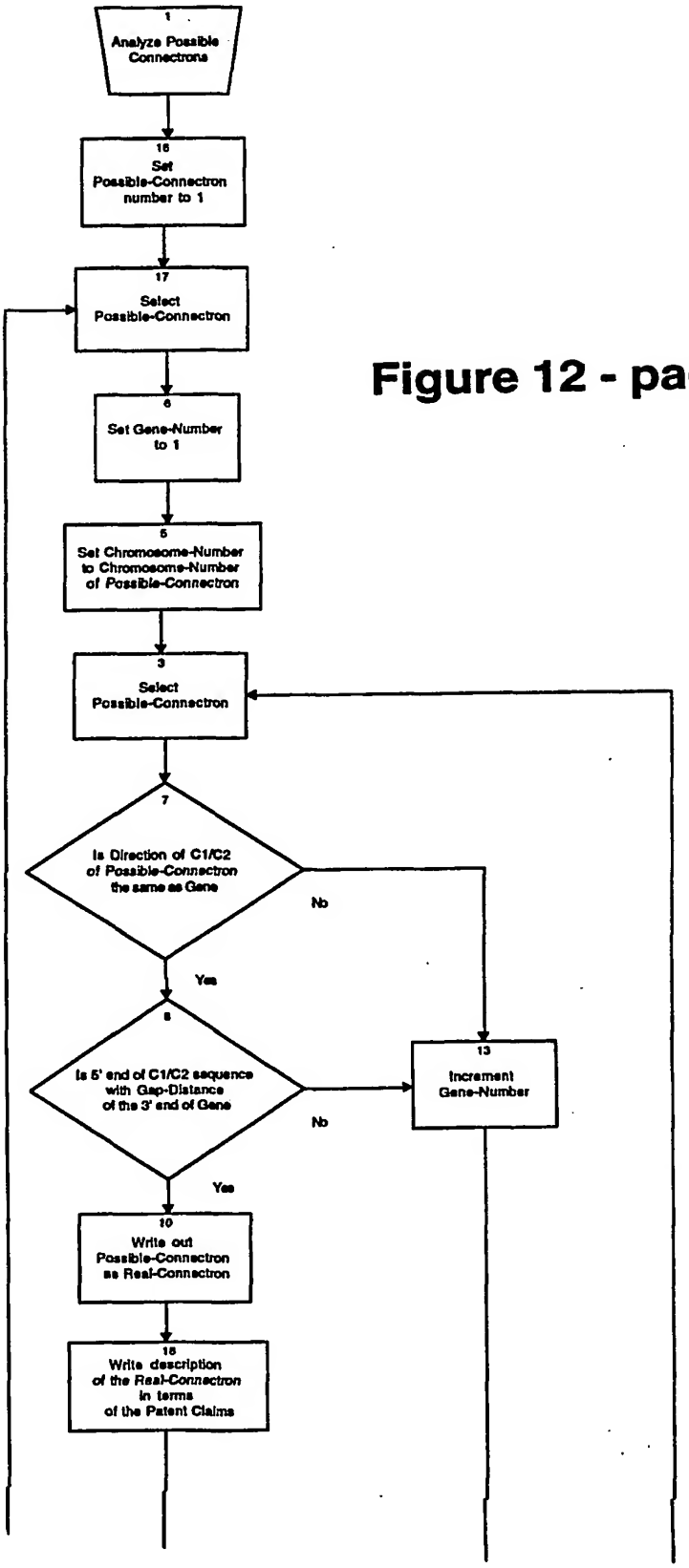


Figure 12 - page 1

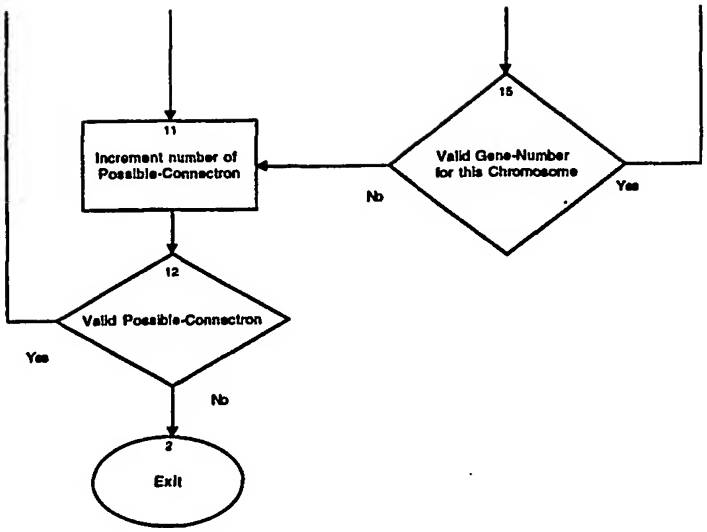


Figure 12 - page 2

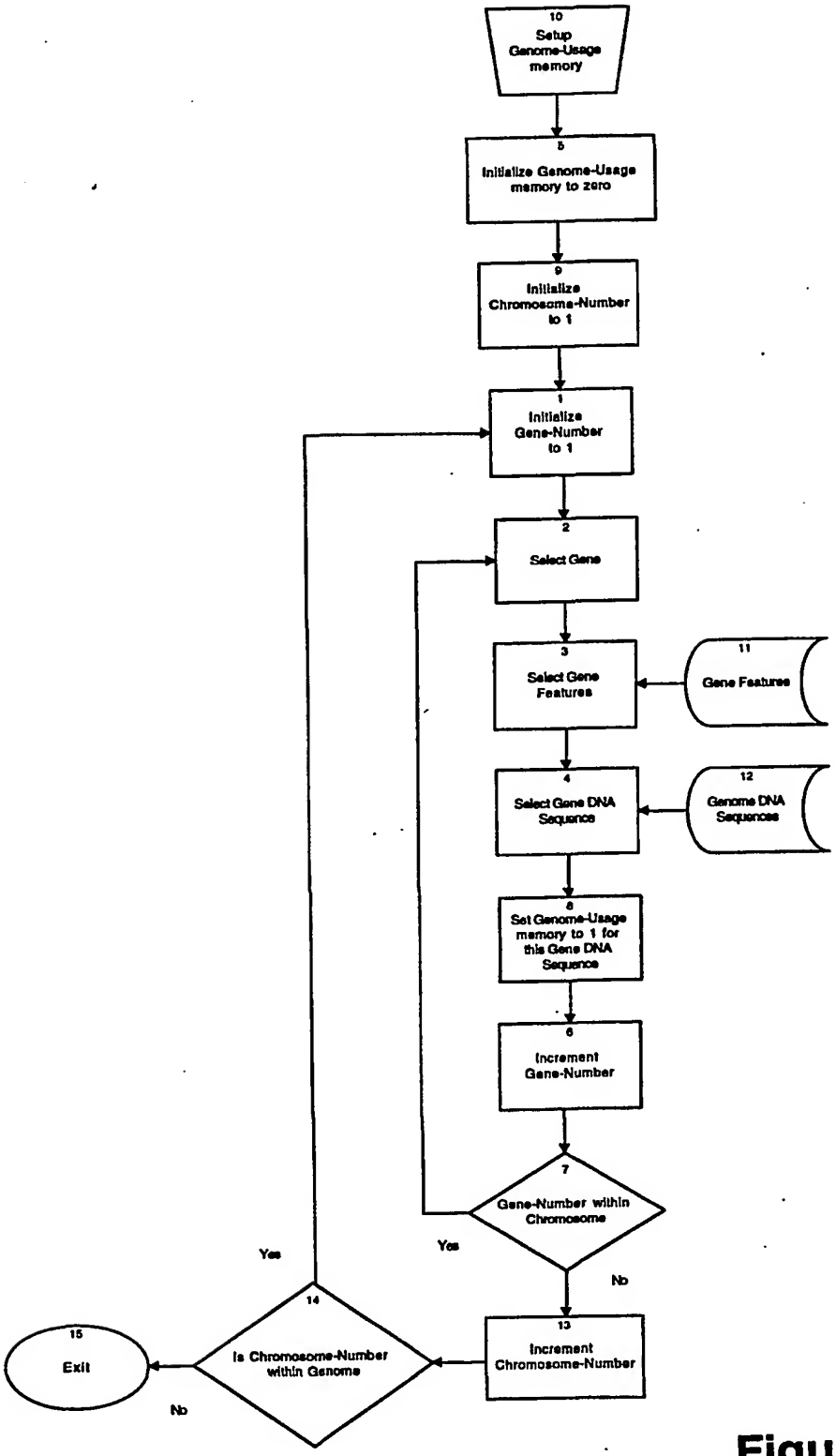


Figure 13

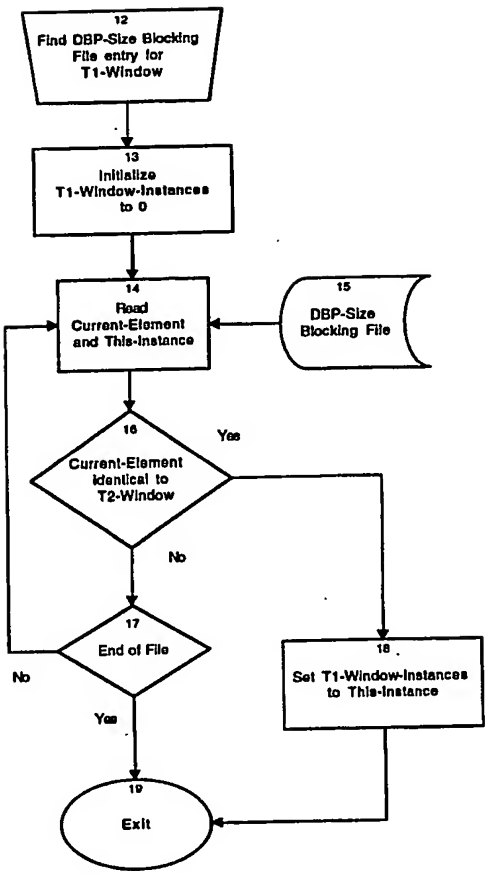

12
Find DBP-Size Blocking File entry for T1-Window
13
Initialize T1-Window-Instances to 0
14
Read Current-Element and This-Instance
15
DBP-Size Blocking File
16
Current-Element identical to T2-Window
Yes
No
17
End of File
No
Yes
18
Set T1-Window-Instances to This-Instance
19
Exit

Figure 14

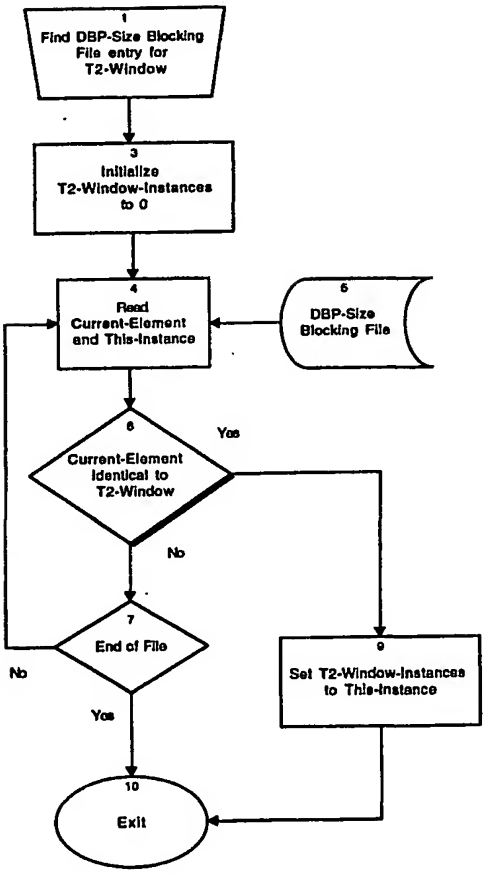


Figure 15

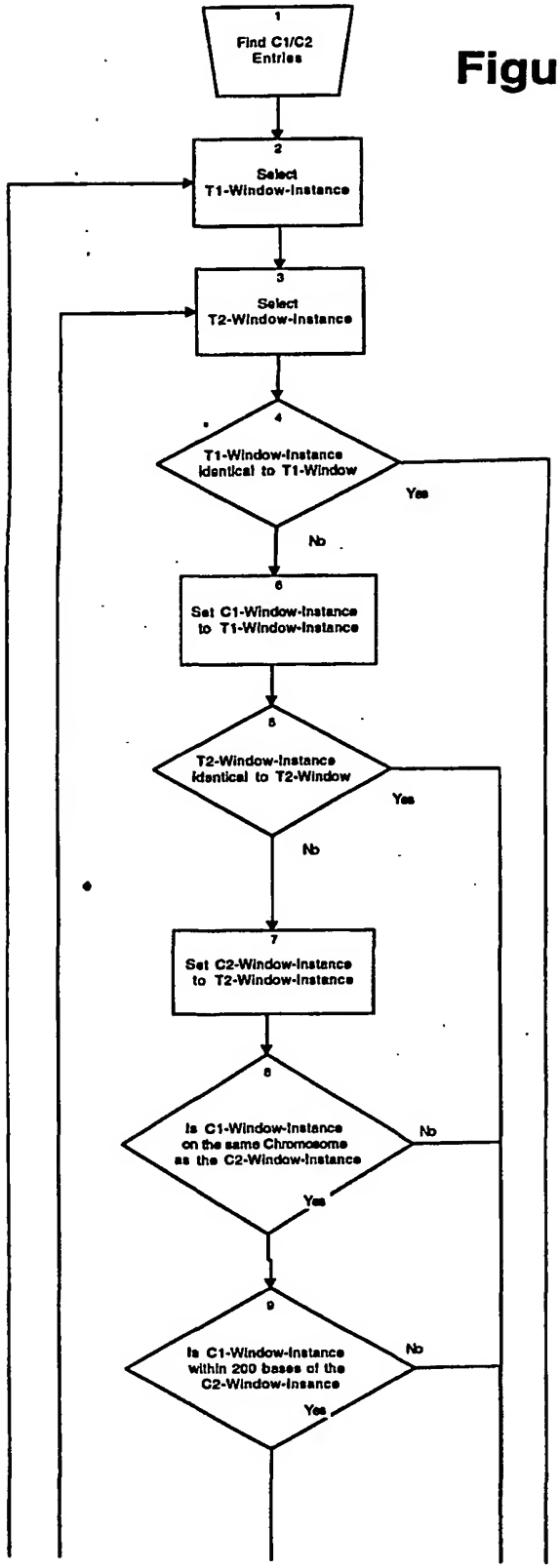


Figure 16 - page 1

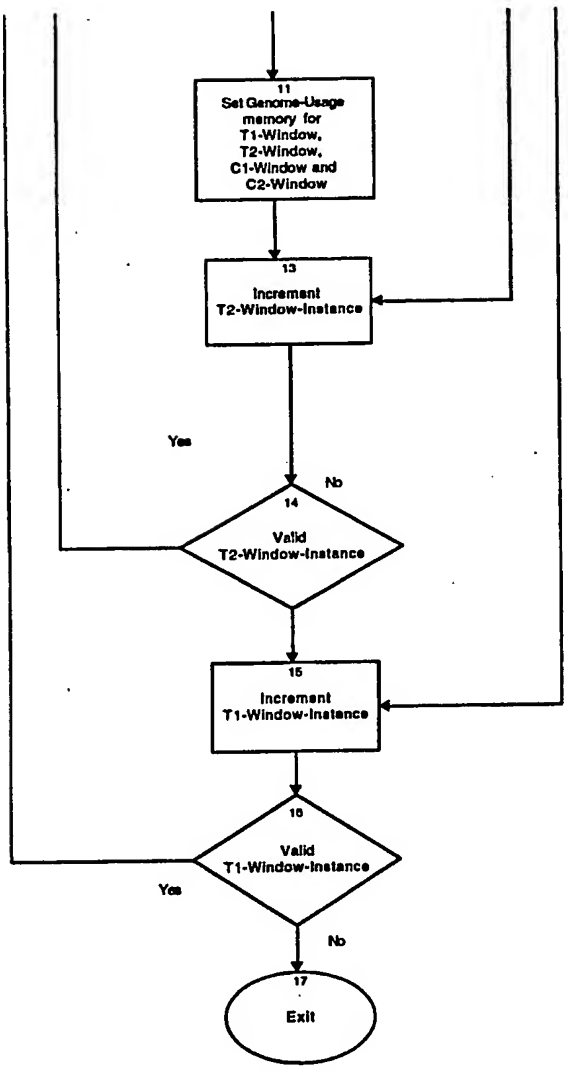


Figure 16 - page 2

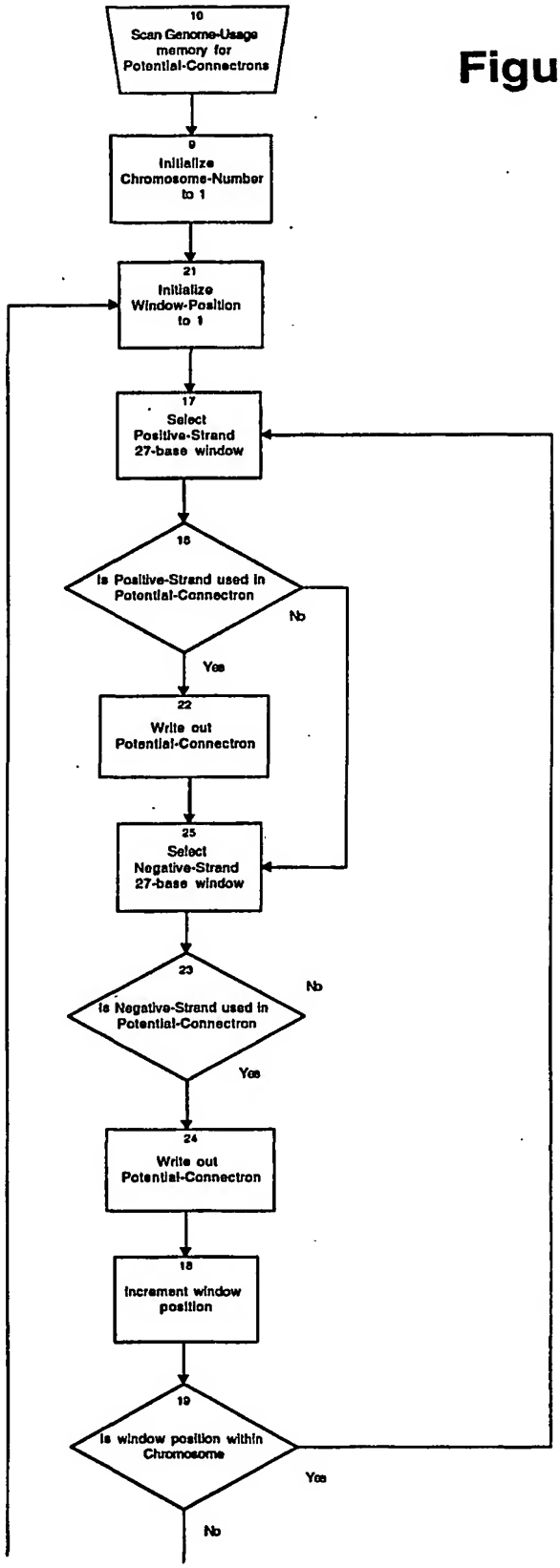


Figure 17 - page 1

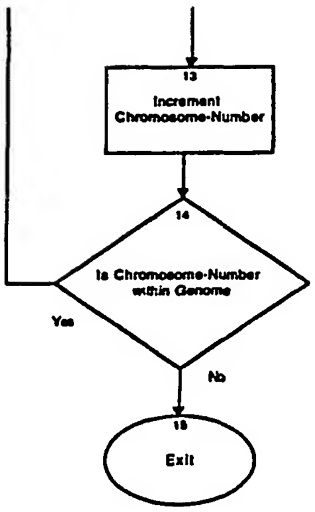


Figure 17 - page 2

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(25) Filing Language: English

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09/866,925 30 May 2001 (30.05.2001) US

(71) Applicant: GLOBAL DETERMINANTS, INC. [US/US]; 17800 Mill Creek Drive, Derwood, MD 20855-1019 (US).

(72) Inventor: FELDMANN, Richard, J.; 17800 Mill Creek Drive, Derwood, MD 20855-1019 (US).

(74) Agent: ZEGEER, Jim; 801 North Pitt Street #108, Alexandria, VA 22314 (US).

(81) Designated States *(national)*: AU, CA, IL, JP, MX.

(84) Designated States *(regional)*: European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR).

Published:
— *with international search report*

(88) Date of publication of the international search report:
18 April 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/94542 A3

(54) Title: ALGORITHMIC DETERMINATION OF CONNECTRONS

(57) Abstract: An algorithm has been developed to identify four DNA sequences of 20 bases or more that form a structure called a connectron. Two sequences C1 and C2 are expressed as RNA in the 3'UTR of some genes in many prokaryotic, archea and eukaryotic genomes. The other half of a connectron is two DNA sequences T1 and T2 that are 1kb to 105kb apart on the same chromosome. The C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. C1/C2 and T1-T2 can be on different chromosomes. The C1/C2 RNA sequence of the gene transcript forms a triple-stranded Hoogsteen helix with the double-stranded T1 and T2 DNA sequences. The formation of connectrons blocks expression of genes between T1 and T2.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/16471

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : G06F 19/00
US CL : 702/19

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 702/19

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KAIN et al. in Current Protocols in Molecular Biology, Ausubel et al. Eds. New York:John Wiley and Sons. 1996, pages 9.6.1 to 9.6.12, especially page 9.6.3.	1
X	ZHANG et al. Identification of Human Gene core Promoters in Silico. Genome Research. 1998, Vol. 8, pages 319-326, especially page 319.	2
A	Matzke et al. How and Why Do Plants Inactivate Homologous (Trans)genes? Plant Physiology. 1995, Vol. 107, pages 679-685, especially page 681.	3-18
A	Fire et al. Potent and specific genetic interference by double-stranded RNA in Caenorabditis elegans. Nature. 19 February 1998, Vol. 391, pages 806-811, especially pages 806-807.	3-18

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
15 August 2001 (15.08.2001)	23 JAN 2002
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer John S. Brusca, Ph.D. Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/16471

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☒ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/16471

Continuation of Item 4 of the first sheet:
The title does not comply with PCT Rule 4.3 because it is longer than 7 words. The new title is as follows:

Algorithmic determination of connectrons.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1, drawn to a promoter detection comprising exclusion of introns and exons.

Group II, claim(s) 2, drawn to a promoter detection method comprising detection of DNA linked to RNA.

Group III, claim(s) 3, drawn to a promoter detection method comprising detection of connectron behavior.

Group IV, claim(s) 4, drawn to a method of modifying expression comprising detection of changes in connectron behavior.

Group V, claim(s) 5, drawn to a method of detecting integration by detection of connectrons.

Group VI, claim(s) 6, drawn to a method of detecting expression of genes by detecting flow of connectrons.

Group VII, claim(s) 7, drawn to a method of modifying a body by modification of connectrons.

Group VIII, claim(s) 8, drawn to a method of detection of connectrons by any of three methods:a) determining base composition, b) determining one of more sites of control sequence organization, and c) determining sites of target application.

Group IX, claim(s) 9, drawn to a method of determining cell response by use of complete genome sequences and detection of changes in connectrons caused by stimulus to the genome.

Group X, claim(s) 10, drawn to polynucleotides with a defined symmetry.

Group XI, claim(s) 11, drawn to polynucleoti8des with a first connectron relationship.

Group XII, claim(s) 12, drawn to polynucleotides with a second connectron relationship.

Group XIII, claim(s) 13, drawn to polynucleotides with a third connectron relationship.

Group XIV, claim(s) 14, drawn to polynucleotides with a fourth connectron relationship of plants and higher animals.

Group XV, claim(s) 15, drawn to polynucleotides with a fifth connectron relationship.

Group XVI, claim(s) 16, drawn to polynucleotides with a sixth connectron relationship.

Group XVII, claim(s) 17, drawn to polynucleotides with a seventh connectron relationship.

Group XVIII, claim(s) 18, drawn to polynucleotides with an eighth connectron relationship.

Group XIX, claim(s) 19, drawn to polynucleotides with a ninth connectron relationship.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

Group VIII is drawn to three species of detection of connectrons comprising the alternative steps of: 1) determining base composition, 2) determining one or more sites of control sequence organization, and 3) determining sites of target application.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/16471

The claims are deemed to correspond to the species listed above in the following manner:

The following claim(s) are generic: 8.

The inventions listed as Groups 1-19 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: PCT Rule 13.1 and Annex B do not provide for unity of invention between two or more different products or methods of use that share a special technical feature. To the extent the groups have a special technical feature of a connectron, the groups are drawn to different methods of use or detection of connectrons. To the extent the groups are drawn to compositions of connectrons, the groups are drawn to compositions with different structures that lack a common special technical feature.

The species listed above do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: The species listed for Group VIII are drawn to three different methods with different steps that produce different results.

Continuation of B. FIELDS SEARCHED Item 3:
Medline, Biosis, US Patent, Derwent World Patent Index
search terms:promoter, software, connectron